



SEQUENCE LISTING

<110> HIRANO, SEIKO
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<120> GENES FOR HEAT RESISTANT ENZYMES OF AMINO ACID BIOSYNTHETIC
PATHWAY DERIVED FROM THERMOPHILIC CORYNEFORM BACTERIA

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<141> 2002-04-03

<150> PCT/JP00/06913

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<150> JP 11-311147

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Met	Gln	Gly	Thr	Val	Ile	Lys	Val	Asn	Val	Glu	Asp	Gly	Ala	Glu	Val		
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Ser	Glu	Gly	Asp	Thr	Val	Val	Val	Leu	Glu	Ala	Met	Lys	Met	Glu	Asn		
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Pro	Val	Lys	Ala	His	Lys	Ser	Gly	Thr	Val	Ser	Gly	Leu	Thr	Ile	Ala		
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 <213> Corynebacterium thermoaminogenes

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 caccgcgttc cccaccgtgg acacggcatt gatccgacac ggtggggata gtttcatgct 240
 gaaaaactat cgctgtgcag ggaggatccg gaatgtgacc tatttcatgg agaaatgatt 300
 gtggacgata cccccgggta cggtaccat tccaaaac atg acc att tcc tca cct 356
 Met Thr Ile Ser Ser Pro
 1 5
 ttg att gac gtc gct aac ctg cca gac atc aac acc acc gcc ggc aag 404
 Leu Ile Asp Val Ala Asn Leu Pro Asp Ile Asn Thr Thr Ala Gly Lys
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 atc gcc gac ctg aag gcc cgc cgg gcg gaa gcc cac ttc ccc atg ggt 452
 Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu Ala His Phe Pro Met Gly
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 gaa aag gcc gta gag aag gtc cac gcg gcc aac cgc ctc acc gcg cgc 500
 Glu Lys Ala Val Glu Lys Val His Ala Ala Asn Arg Leu Thr Ala Arg
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 gaa cga ctt gac tac ctg ctc gat gaa ggc tcc ttc atc gaa acc gat 548
 Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly Ser Phe Ile Glu Thr Asp
 55 60 65 70
 cag ctc gca cgc cac cgc acc acc gcg ttc ggc ctg ggc aac aag cga 596
 Gln Leu Ala Arg His Arg Thr Thr Ala Phe Gly Leu Gly Asn Lys Arg
 75 80 85
 ccg gcc acc gac ggc atc gtc acc ggc tgg ggc acc atc gac ggc cgc 644
 Pro Ala Thr Asp Gly Ile Val Thr Gly Trp Gly Thr Ile Asp Gly Arg
 90 95 100
 gag gtc tgc atc ttc tcc cag gac ggc acc gtc ttc ggt ggc gca ctc 692

Glu	Val	Cys	Ile	Phe	Ser	Gln	Asp	Gly	Thr	Val	Phe	Gly	Gly	Ala	Leu	
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ggt	gag	gtc	tac	ggc	gag	aag	atg	atc	aag	atc	atg	gag	ctg	gcc	atc	740
Gly	Glu	Val	Tyr	Gly	Glu	Lys	Met	Ile	Lys	Ile	Met	Glu	Leu	Ala	Ile	
		120					125					130				
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Asp	Thr	Gly	Arg	Pro	Leu	Ile	Gly	Leu	Tyr	Glu	Gly	Ala	Gly	Ala	Arg	
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atc	cag	gac	ggt	gcg	gtc	tcc	ctc	gac	ttc	atc	tcc	cag	acc	ttc	tat	836
Ile	Gln	Asp	Gly	Ala	Val	Ser	Leu	Asp	Phe	Ile	Ser	Gln	Thr	Phe	Tyr	
				155					160					165		
cag	aac	atc	cag	gcc	tcc	ggc	gtg	atc	ccg	cag	atc	tcc	gtg	atc	atg	884
Gln	Asn	Ile	Gln	Ala	Ser	Gly	Val	Ile	Pro	Gln	Ile	Ser	Val	Ile	Met	
			170					175					180			
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Gly	Ala	Cys	Ala	Gly	Gly	Asn	Ala	Tyr	Gly	Pro	Ala	Leu	Thr	Asp	Phe	
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Val	Val	Met	Val	Asp	Lys	Thr	Ser	Lys	Met	Phe	Val	Thr	Gly	Pro	Asp	
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Val	Ile	Lys	Thr	Val	Thr	Gly	Glu	Glu	Ile	Thr	Gln	Glu	Glu	Leu	Gly	
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gga	gca	acc	acc	cac	atg	gtc	acc	gcc	ggc	aac	tcc	cac	tac	acc	gtc	1076
Gly	Ala	Thr	Thr	His	Met	Val	Thr	Ala	Gly	Asn	Ser	His	Tyr	Thr	Val	
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gcc	acc	gat	gag	gag	gcc	ctc	gac	tgg	gtc	cag	gac	ctc	atc	tcc	ttc	1124
Ala	Thr	Asp	Glu	Glu	Ala	Leu	Asp	Trp	Val	Gln	Asp	Leu	Ile	Ser	Phe	
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ctg	ccc	tcc	aac	aat	cgc	tcc	tac	gcc	ccg	gtg	gag	gag	ttc	gac	gag	1172
Leu	Pro	Ser	Asn	Asn	Arg	Ser	Tyr	Ala	Pro	Val	Glu	Glu	Phe	Asp	Glu	
		265				270						275				
gag	gac	ggt	ggc	atc	gcc	gag	aac	atc	acc	gcc	gat	gac	ctg	aag	ctg	1220
Glu	Asp	Gly	Gly	Ile	Ala	Glu	Asn	Ile	Thr	Ala	Asp	Asp	Leu	Lys	Leu	
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gat	gag	atc	atc	ccg	gat	tcc	gcc	acc	gtg	ccc	tat	gat	gtc	cgc	gac	1268
Asp	Glu	Ile	Ile	Pro	Asp	Ser	Ala	Thr	Val	Pro	Tyr	Asp	Val	Arg	Asp	
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gtc	atc	cag	tgc	ctg	acc	gac	gac	ggt	gag	tac	ctg	gag	atc	cag	gcc	1316
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gac	cga	gcc	gag	aat	gtc	gtc	atc	gcc	ttc	ggc	cgc	atc	gag	ggc	cag	1364
Asp	Arg	Ala	Glu	Asn	Val	Val	Ile	Ala	Phe	Gly	Arg	Ile	Glu	Gly	Gln	
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tcc	gtc	ggt	ttc	gtc	gcc	aac	cag	ccg	acc	cag	ttc	gcc	ggc	tgc	ctg	1412
Ser	Val	Gly	Phe	Val	Ala	Asn	Gln	Pro	Thr	Gln	Phe	Ala	Gly	Cys	Leu	
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gac	atc	gac	tcc	tcc	gag	aag	gca	gcc	cgc	ttc	gtc	cgc	acc	tgc	gat	1460
Asp	Ile	Asp	Ser	Ser	Glu	Lys	Ala	Ala	Arg	Phe	Val	Arg	Thr	Cys	Asp	
		360				365					370					
gcc	ttc	aac	atc	ccg	atc	gtc	atg	ctt	gtc	gac	gtc	ccc	ggc	ttc	ctc	1508

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ccc	ggt	gcc	ggc	cag	gag	tac	ggc	ggc	atc	ctg	cgt	cgt	ggc	gcc	aaa	1556								
Pro	Gly	Ala	Gly	Gln	Glu	Tyr	Gly	Gly	Ile	Leu	Arg	Arg	Gly	Ala	Lys									
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Leu	Leu	Tyr	Ala	Tyr	Gly	Glu	Ala	Thr	Val	Pro	Lys	Ile	Thr	Val	Thr									
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Met	Arg	Lys	Ala	Tyr	Gly	Gly	Ala	Tyr	Cys	Val	Met	Gly	Ser	Lys	Gly									
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	440					445					450													
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Met	Gly	Ala	Ala	Gly	Ala	Val	Gln	Phe	Ile	Tyr	Arg	Lys	Glu	Leu	Met									
455					460					465				470										
gcc	gct	gat	gcc	aag	ggc	ctg	gac	acc	gtc	gcc	ctg	gcc	cag	tcc	ttc	1796								
Ala	Ala	Asp	Ala	Lys	Gly	Leu	Asp	Thr	Val	Ala	Leu	Ala	Gln	Ser	Phe									
				475					480					485										
gag	cgt	gag	tac	gag	gac	cac	atg	ctc	aac	ccg	tac	ctg	gcg	gcc	gag	1844								
Glu	Arg	Glu	Tyr	Glu	Asp	His	Met	Leu	Asn	Pro	Tyr	Leu	Ala	Ala	Glu									
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Arg	Gly	Leu	Ile	Asp	Ala	Val	Ile	Leu	Pro	Ser	Glu	Thr	Arg	Gly	Gln									
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Ile	Ala	Arg	Asn	Leu	Arg	Leu	Leu	Lys	His	Lys	Asn	Val	Ser	Arg	Pro									
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gcc	cgc	aag	cac	ggc	aac	atg	cca	ctg	taagcaccgcg ggaccacccc						1987									
Ala	Arg	Lys	His	Gly	Asn	Met	Pro	Leu																
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<211> 543

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 6

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Ala	His	Phe	Pro	Met	Gly	Glu	Lys	Ala	Val	Glu	Lys	Val	His	Ala	Ala		
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Asn	Arg	Leu	Thr	Ala	Arg	Glu	Arg	Leu	Asp	Tyr	Leu	Leu	Asp	Glu	Gly		
	50					55					60						
Ser	Phe	Ile	Glu	Thr	Asp	Gln	Leu	Ala	Arg	His	Arg	Thr	Thr	Ala	Phe		

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Gly	Leu	Gly	Asn	Lys	Arg	Pro	Ala	Thr	Asp	Gly	Ile	Val	Thr	Gly	Trp
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Gly	Thr	Ile	Asp	Gly	Arg	Glu	Val	Cys	Ile	Phe	Ser	Gln	Asp	Gly	Thr
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Val	Phe	Gly	Gly	Ala	Leu	Gly	Glu	Val	Tyr	Gly	Glu	Lys	Met	Ile	Lys
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Ile	Met	Glu	Leu	Ala	Ile	Asp	Thr	Gly	Arg	Pro	Leu	Ile	Gly	Leu	Tyr
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Ile	Ser	Gln	Thr	Phe	Tyr	Gln	Asn	Ile	Gln	Ala	Ser	Gly	Val	Ile	Pro
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Gln	Ile	Ser	Val	Ile	Met	Gly	Ala	Cys	Ala	Gly	Gly	Asn	Ala	Tyr	Gly
		180						185					190		
Pro	Ala	Leu	Thr	Asp	Phe	Val	Val	Met	Val	Asp	Lys	Thr	Ser	Lys	Met
		195					200						205		
Phe	Val	Thr	Gly	Pro	Asp	Val	Ile	Lys	Thr	Val	Thr	Gly	Glu	Glu	Ile
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Thr	Gln	Glu	Glu	Leu	Gly	Gly	Ala	Thr	Thr	His	Met	Val	Thr	Ala	Gly
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Asn	Ser	His	Tyr	Thr	Val	Ala	Thr	Asp	Glu	Glu	Ala	Leu	Asp	Trp	Val
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Gln	Asp	Leu	Ile	Ser	Phe	Leu	Pro	Ser	Asn	Asn	Arg	Ser	Tyr	Ala	Pro
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Val	Glu	Glu	Phe	Asp	Glu	Glu	Asp	Gly	Gly	Ile	Ala	Glu	Asn	Ile	Thr
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Ala	Asp	Asp	Leu	Lys	Leu	Asp	Glu	Ile	Ile	Pro	Asp	Ser	Ala	Thr	Val
	290					295					300				
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Tyr	Leu	Glu	Ile	Gln	Ala	Asp	Arg	Ala	Glu	Asn	Val	Val	Ile	Ala	Phe
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Gln	Phe	Ala	Gly	Cys	Leu	Asp	Ile	Asp	Ser	Ser	Glu	Lys	Ala	Ala	Arg
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Phe	Val	Arg	Thr	Cys	Asp	Ala	Phe	Asn	Ile	Pro	Ile	Val	Met	Leu	Val
	370					375					380				
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385					390					395					400
Leu	Arg	Arg	Gly	Ala	Lys	Leu	Leu	Tyr	Ala	Tyr	Gly	Glu	Ala	Thr	Val
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Pro	Lys	Ile	Thr	Val	Thr	Met	Arg	Lys	Ala	Tyr	Gly	Gly	Ala	Tyr	Cys
			420					425					430		
Val	Met	Gly	Ser	Lys	Gly	Leu	Gly	Ala	Asp	Ile	Asn	Leu	Ala	Trp	Pro
	435						440					445			
Thr	Ala	Gln	Ile	Ala	Val	Met	Gly	Ala	Ala	Gly	Ala	Val	Gln	Phe	Ile
	450					455					460				
Tyr	Arg	Lys	Glu	Leu	Met	Ala	Ala	Asp	Ala	Lys	Gly	Leu	Asp	Thr	Val
465					470					475					480

Ala	Leu	Ala	Gln	Ser	Phe	Glu	Arg	Glu	Tyr	Glu	Asp	His	Met	Leu	Asn
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Pro	Tyr	Leu	Ala	Ala	Glu	Arg	Gly	Leu	Ile	Asp	Ala	Val	Ile	Leu	Pro
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Ser	Glu	Thr	Arg	Gly	Gln	Ile	Ala	Arg	Asn	Leu	Arg	Leu	Leu	Lys	His
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<220>
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Ala Ala Thr Thr Ala Pro Asp Leu Thr Thr Thr Ala Gly Lys Leu Ala						
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Asp Leu Arg Ala Arg Leu Ser Glu Thr Gln Ala Pro Met Gly Gln Ala						
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tcc gtg gag aag gtg cac gag gca ggg aag aag acc gca cgc gag cgc	561					
Ser Val Glu Lys Val His Glu Ala Gly Lys Lys Thr Ala Arg Glu Arg						
35 40 45 50						
atc gag tac ctg ctc gat gag ggc tcc ttc gtt gag gtc gat gcc ctc	609					
Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Val Asp Ala Leu						
55 60 65						
gcc cgc cac cgt tcc aag aac ttc ggc ctg gac tcc aag cgc ccg gtc	657					
Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ser Lys Arg Pro Val						
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acc gac ggt gtg gtc acc ggt tac ggc acc atc gac gga cgc aag gtc	705					
Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg Lys Val						
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tgc gtc ttc tcc cag gac ggc gct atc ttc ggc ggt gcc ctc ggt gag	753					
Cys Val Phe Ser Gln Asp Gly Ala Ile Phe Gly Gly Ala Leu Gly Glu						
100 105 110						
gtc tac ggc gag aag atc gtc aag atc atg gac ctg gcc atc aag acc	801					
Val Tyr Gly Glu Lys Ile Val Lys Ile Met Asp Leu Ala Ile Lys Thr						

115					120					125					130	
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Gly	Val	Pro	Leu	Ile	Gly	Ile	Asn	Glu	Gly	Ala	Gly	Ala	Arg	Ile	Gln	
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gaa	ggc	gtt	gtc	tcc	ctg	ggc	ctg	tac	tcc	cag	atc	ttc	tac	cgc	aac	897
Glu	Gly	Val	Val	Ser	Leu	Gly	Leu	Tyr	Ser	Gln	Ile	Phe	Tyr	Arg	Asn	
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Thr	Gln	Ala	Ser	Gly	Val	Ile	Pro	Gln	Ile	Ser	Leu	Ile	Met	Gly	Ala	
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Cys	Ala	Gly	Gly	His	Val	Tyr	Ser	Pro	Ala	Leu	Thr	Asp	Phe	Ile	Ile	
	180					185					190					
atg	gtg	gac	aag	acc	tcc	aag	atg	ttc	atc	acc	ggc	ccc	gac	gtg	atc	1041
Met	Val	Asp	Lys	Thr	Ser	Lys	Met	Phe	Ile	Thr	Gly	Pro	Asp	Val	Ile	
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Lys	Thr	Val	Thr	Gly	Glu	Glu	Val	Thr	Gln	Glu	Glu	Leu	Gly	Gly	Ala	
			215						220					225		
tac	acc	cac	atg	gcc	cag	tcc	ggc	acc	tcg	cac	tac	acc	gca	gcc	gat	1137
Tyr	Thr	His	Met	Ala	Gln	Ser	Gly	Thr	Ser	His	Tyr	Thr	Ala	Ala	Asp	
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gac	tcc	gat	gcc	ctc	gac	tgg	gtc	cgt	gag	ctg	gtc	agc	tac	ctg	ccg	1185
Asp	Ser	Asp	Ala	Leu	Asp	Trp	Val	Arg	Glu	Leu	Val	Ser	Tyr	Leu	Pro	
		245					250					255				
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Ser	Asn	Asn	Arg	Ala	Glu	Thr	Pro	Arg	Gln	Asp	Ala	Asp	Ile	Met	Val	
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ggc	tcc	atc	aag	gag	aac	atc	acc	gag	acc	gac	ctc	gaa	ctc	gac	acc	1281
Gly	Ser	Ile	Lys	Glu	Asn	Ile	Thr	Glu	Thr	Asp	Leu	Glu	Leu	Asp	Thr	
275					280					285					290	
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Leu	Ile	Pro	Asp	Ser	Pro	Asn	Gln	Pro	Tyr	Asp	Met	Lys	Asp	Val	Ile	
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Thr	Arg	Ile	Val	Asp	Asp	Ala	Glu	Phe	Phe	Glu	Ile	Gln	Glu	Gly	Tyr	
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Ala	Glu	Asn	Ile	Ile	Cys	Gly	Phe	Ala	Arg	Val	Glu	Gly	Arg	Ala	Val	
		325				330						335				
ggt	atc	gtg	gcc	aac	cag	ccg	atg	cag	ttc	gcc	ggc	tgc	ctg	gac	atc	1473
Gly	Ile	Val	Ala	Asn	Gln	Pro	Met	Gln	Phe	Ala	Gly	Cys	Leu	Asp	Ile	
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Lys	Ala	Ser	Glu	Lys	Ala	Ala	Arg	Phe	Ile	Arg	Thr	Cys	Asp	Ala	Phe	
355					360					365					370	
aac	atc	ccg	atc	atc	gag	ctt	gtc	gac	gtc	cca	ggc	ttc	ctc	ccg	ggc	1569
Asn	Ile	Pro	Ile	Ile	Glu	Leu	Val	Asp	Val	Pro	Gly	Phe	Leu	Pro	Gly	
			375				380							385		
acc	aac	cag	gag	ttc	gac	ggc	atc	atc	cgt	cgc	ggc	gcg	aag	ctg	ctc	1617
Thr	Asn	Gln	Glu	Phe	Asp	Gly	Ile	Ile	Arg	Arg	Gly	Ala	Lys	Leu	Leu	

	390		395		400		
tac gcc tac gcc gag gcc acc gtc ggc aag atc acc gtg atc acc cgc						1665	
Tyr Ala Tyr Ala Glu Ala Thr Val Gly Lys Ile Thr Val Ile Thr Arg							
	405		410		415		
aag tcc tac ggc ggt gcc tac tgc gtg atg ggc tcc aag gac atg ggt						1713	
Lys Ser Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Asp Met Gly							
	420		425		430		
gcg gac ctc gtc ttc gca tgg ccc acc gcg cag atc gcc gtc atg ggt						1761	
Ala Asp Leu Val Phe Ala Trp Pro Thr Ala Gln Ile Ala Val Met Gly							
	435		440		445		450
gcc tcc ggt gcc gtc ggc ttc atc tac cgc aag gag ctc aag cag gct						1809	
Ala Ser Gly Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Lys Gln Ala							
	455		460		465		
gca gcg gcc ggc gag gat gtc acc gcg ctg atg aag aag tac gag cag						1857	
Ala Ala Ala Gly Glu Asp Val Thr Ala Leu Met Lys Lys Tyr Glu Gln							
	470		475		480		
gag tac gag gag acc ctg gtc aac ccg tac atg gct gca gag cgt ggc						1905	
Glu Tyr Glu Glu Thr Leu Val Asn Pro Tyr Met Ala Ala Glu Arg Gly							
	485		490		495		
tac gtc gac gcc gtc atc cca cca tcc gag acc cgt ggt cag atc atc						1953	
Tyr Val Asp Ala Val Ile Pro Pro Ser Glu Thr Arg Gly Gln Ile Ile							
	500		505		510		
gag ggt ctg cgt ctg ctc gac cgc aag gtg gtc aac gtc ccg gcc aag						2001	
Glu Gly Leu Arg Leu Leu Asp Arg Lys Val Val Asn Val Pro Ala Lys							
	515		520		525		530
aag cac ggt aac atc ccg ctg taaaccgtct tcccctccgg caccacgccg						2052	
Lys His Gly Asn Ile Pro Leu							
	535						
gagaaggctt tgtccgcagc tgtc						2076	

<210> 8
 <211> 537
 <212> PRT
 <213> Corynebacterium thermoaminogenes

<400> 8
 Met Thr Ala Ala Thr Thr Ala Pro Asp Leu Thr Thr Thr Ala Gly Lys
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 Leu Ala Asp Leu Arg Ala Arg Leu Ser Glu Thr Gln Ala Pro Met Gly
 20 25 30
 Gln Ala Ser Val Glu Lys Val His Glu Ala Gly Lys Lys Thr Ala Arg
 35 40 45
 Glu Arg Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Val Asp
 50 55 60
 Ala Leu Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ser Lys Arg
 65 70 75 80
 Pro Val Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg
 85 90 95
 Lys Val Cys Val Phe Ser Gln Asp Gly Ala Ile Phe Gly Gly Ala Leu
 100 105 110
 Gly Glu Val Tyr Gly Glu Lys Ile Val Lys Ile Met Asp Leu Ala Ile

		115					120				125				
Lys	Thr	Gly	Val	Pro	Leu	Ile	Gly	Ile	Asn	Glu	Gly	Ala	Gly	Ala	Arg
	130					135					140				
Ile	Gln	Glu	Gly	Val	Val	Ser	Leu	Gly	Leu	Tyr	Ser	Gln	Ile	Phe	Tyr
145					150					155					160
Arg	Asn	Thr	Gln	Ala	Ser	Gly	Val	Ile	Pro	Gln	Ile	Ser	Leu	Ile	Met
				165					170						175
Gly	Ala	Cys	Ala	Gly	Gly	His	Val	Tyr	Ser	Pro	Ala	Leu	Thr	Asp	Phe
			180					185					190		
Ile	Ile	Met	Val	Asp	Lys	Thr	Ser	Lys	Met	Phe	Ile	Thr	Gly	Pro	Asp
		195					200					205			
Val	Ile	Lys	Thr	Val	Thr	Gly	Glu	Glu	Val	Thr	Gln	Glu	Glu	Leu	Gly
	210					215					220				
Gly	Ala	Tyr	Thr	His	Met	Ala	Gln	Ser	Gly	Thr	Ser	His	Tyr	Thr	Ala
225					230					235					240
Ala	Asp	Asp	Ser	Asp	Ala	Leu	Asp	Trp	Val	Arg	Glu	Leu	Val	Ser	Tyr
				245					250					255	
Leu	Pro	Ser	Asn	Asn	Arg	Ala	Glu	Thr	Pro	Arg	Gln	Asp	Ala	Asp	Ile
			260					265					270		
Met	Val	Gly	Ser	Ile	Lys	Glu	Asn	Ile	Thr	Glu	Thr	Asp	Leu	Glu	Leu
		275					280					285			
Asp	Thr	Leu	Ile	Pro	Asp	Ser	Pro	Asn	Gln	Pro	Tyr	Asp	Met	Lys	Asp
	290					295					300				
Val	Ile	Thr	Arg	Ile	Val	Asp	Asp	Ala	Glu	Phe	Phe	Glu	Ile	Gln	Glu
305					310					315					320
Gly	Tyr	Ala	Glu	Asn	Ile	Ile	Cys	Gly	Phe	Ala	Arg	Val	Glu	Gly	Arg
				325					330					335	
Ala	Val	Gly	Ile	Val	Ala	Asn	Gln	Pro	Met	Gln	Phe	Ala	Gly	Cys	Leu
			340					345					350		
Asp	Ile	Lys	Ala	Ser	Glu	Lys	Ala	Ala	Arg	Phe	Ile	Arg	Thr	Cys	Asp
		355					360					365			
Ala	Phe	Asn	Ile	Pro	Ile	Ile	Glu	Leu	Val	Asp	Val	Pro	Gly	Phe	Leu
	370					375					380				
Pro	Gly	Thr	Asn	Gln	Glu	Phe	Asp	Gly	Ile	Ile	Arg	Arg	Gly	Ala	Lys
385					390					395					400
Leu	Leu	Tyr	Ala	Tyr	Ala	Glu	Ala	Thr	Val	Gly	Lys	Ile	Thr	Val	Ile
				405					410					415	
Thr	Arg	Lys	Ser	Tyr	Gly	Gly	Ala	Tyr	Cys	Val	Met	Gly	Ser	Lys	Asp
			420					425					430		
Met	Gly	Ala	Asp	Leu	Val	Phe	Ala	Trp	Pro	Thr	Ala	Gln	Ile	Ala	Val
		435					440					445			
Met	Gly	Ala	Ser	Gly	Ala	Val	Gly	Phe	Ile	Tyr	Arg	Lys	Glu	Leu	Lys
	450						455				460				
Gln	Ala	Ala	Ala	Ala	Gly	Glu	Asp	Val	Thr	Ala	Leu	Met	Lys	Lys	Tyr
465					470					475					480
Glu	Gln	Glu	Tyr	Glu	Glu	Thr	Leu	Val	Asn	Pro	Tyr	Met	Ala	Ala	Glu
				485					490					495	
Arg	Gly	Tyr	Val	Asp	Ala	Val	Ile	Pro	Pro	Ser	Glu	Thr	Arg	Gly	Gln
			500					505					510		
Ile	Ile	Glu	Gly	Leu	Arg	Leu	Leu	Asp	Arg	Lys	Val	Val	Asn	Val	Pro
		515					520					525			

Ala Lys Lys His Gly Asn Ile Pro Leu
 530 535

<210> 9
 <211> 1643
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>
 <221> CDS
 <222> (326)..(1363)

<400> 9
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 tcagccaccc gccgatgaga cctgcagcga caacgggtggc ggtgctgacc tggtcagcgt 120
 ctttgagttt catatccatg tcagacagtc taaccactct ctccgacgcg tccgaacatg 180
 ctgggggtggc ggacaccatg tccgttcggg cggttgccccg acgggggaaa atcgcaggca 240
 gatgtgtccg atgtgggata aaccacccgg ttcgggcgtg tcttcgggat caatggcaca 300
 gcattaaccg tgtgggggggt ttaat atg gga gcc atg cga att gcc act ctc 352
 Met Gly Ala Met Arg Ile Ala Thr Leu
 1 5
 acg tca ggc ggc gac tgc ccc gga ctc aat gct gtc atc agg gga atc 400
 Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val Ile Arg Gly Ile
 10 15 20 25
 gtc cgt acc gca agt aat gaa ttc ggt tcc acc gtc gtg ggt tat cag 448
 Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val Val Gly Tyr Gln
 30 35 40
 gac ggc tgg gag ggc ctg ctg gcg gac cga cgt gtt cag ctc tat gac 496
 Asp Gly Trp Glu Gly Leu Leu Ala Asp Arg Arg Val Gln Leu Tyr Asp
 45 50 55
 gat gag gac atc gac cgc atc ctg ctc cgc ggt gga aca atc ctg ggc 544
 Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly Thr Ile Leu Gly
 60 65 70
 acc ggt cgt ctc cac ccc gac aag ttc aga gcc gga atc gac cag gtc 592
 Thr Gly Arg Leu His Pro Asp Lys Phe Arg Ala Gly Ile Asp Gln Val
 75 80 85
 aag gcg aat ctc gcc gat gcg gga att gac gca ctc atc ccg atc ggt 640
 Lys Ala Asn Leu Ala Asp Ala Gly Ile Asp Ala Leu Ile Pro Ile Gly
 90 95 100 105
 ggc gag ggc acc ctc aag gga gcg aag tgg ctc gcc gac aac ggc atc 688
 Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ala Asp Asn Gly Ile
 110 115 120
 ccc gtg gtc ggt gtc ccg aaa acc atc gac aat gat gtc aac ggc acg 736
 Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp Val Asn Gly Thr
 125 130 135
 gat ttc acc ttc ggt ttc gat tcc gcg gtc tct gtg gcc acc gac gcc 784
 Asp Phe Thr Phe Gly Phe Asp Ser Ala Val Ser Val Ala Thr Asp Ala
 140 145 150
 atc gac cgg ctg cac acc acg gcg gaa tcc cac aac cgt gtg atg atc 832
 Ile Asp Arg Leu His Thr Thr Ala Glu Ser His Asn Arg Val Met Ile
 155 160 165

gtc	gag	gtc	atg	ggc	cgc	cac	gtc	ggg	tgg	atc	gca	ctg	cat	gcc	ggc	880
Val	Glu	Val	Met	Gly	Arg	His	Val	Gly	Trp	Ile	Ala	Leu	His	Ala	Gly	
170					175					180					185	
atg	gcc	ggg	gga	gcc	cac	tac	acc	gtc	atc	ccc	gag	gtg	ccc	ttc	gac	928
Met	Ala	Gly	Gly	Ala	His	Tyr	Thr	Val	Ile	Pro	Glu	Val	Pro	Phe	Asp	
				190					195					200		
atc	tcg	gag	atc	tgc	aag	cgt	atg	gaa	cgt	cgc	ttc	cag	atg	ggg	gag	976
Ile	Ser	Glu	Ile	Cys	Lys	Arg	Met	Glu	Arg	Arg	Phe	Gln	Met	Gly	Glu	
			205					210					215			
aag	tac	ggc	atc	atc	gtc	gtc	gcg	gag	ggg	gcc	ctg	ccc	aag	gag	gga	1024
Lys	Tyr	Gly	Ile	Ile	Val	Val	Ala	Glu	Gly	Ala	Leu	Pro	Lys	Glu	Gly	
		220					225					230				
acc	atg	gag	ctg	cgt	gag	ggg	gag	gtg	gat	cag	ttc	ggg	cac	aag	acc	1072
Thr	Met	Glu	Leu	Arg	Glu	Gly	Glu	Val	Asp	Gln	Phe	Gly	His	Lys	Thr	
	235				240					245						
ttc	acc	ggc	atc	ggc	cag	cag	atc	gcc	gac	gag	gtg	cac	agg	cgt	ctg	1120
Phe	Thr	Gly	Ile	Gly	Gln	Gln	Ile	Ala	Asp	Glu	Val	His	Arg	Arg	Leu	
250				255					260						265	
ggg	cat	gat	gtc	cgc	acc	acg	gtc	ctg	ggc	cat	atc	cag	cgt	ggg	ggc	1168
Gly	His	Asp	Val	Arg	Thr	Thr	Val	Leu	Gly	His	Ile	Gln	Arg	Gly	Gly	
			270					275					280			
acc	ccc	acc	gcc	ttc	gac	cgt	gtc	ctg	gcc	acc	cgg	tac	ggg	gtc	cgc	1216
Thr	Pro	Thr	Ala	Phe	Asp	Arg	Val	Leu	Ala	Thr	Arg	Tyr	Gly	Val	Arg	
			285					290					295			
gcc	gcg	cgt	gcc	tgc	cac	gag	ggg	cag	ttc	aac	acc	gtg	gtc	gcg	ctc	1264
Ala	Ala	Arg	Ala	Cys	His	Glu	Gly	Gln	Phe	Asn	Thr	Val	Val	Ala	Leu	
		300					305					310				
aag	ggg	gag	cgc	atc	cgg	atg	atc	tcc	ttc	gat	gag	gcc	gtg	ggc	acc	1312
Lys	Gly	Glu	Arg	Ile	Arg	Met	Ile	Ser	Phe	Asp	Glu	Ala	Val	Gly	Thr	
	315					320					325					
ctg	aag	aag	gtg	ccg	atg	gaa	cgc	tgg	gtg	acc	gcc	cag	gct	atg	ttc	1360
Leu	Lys	Lys	Val	Pro	Met	Glu	Arg	Trp	Val	Thr	Ala	Gln	Ala	Met	Phe	
330				335				340						345		
ggg	tagtcaggcc	gcattcccgg	ttccgcgccc	gcggggccgg	gttttttcat											1413
Gly																
gccccggaac	acatcggtat	gaaatcgtga	tatgcattac	ttgacgggga	agtgggggat											1473
ccgtcacctc	gcgttgtcca	actacagccc	gcagcgcctg	cggaattct	tcgagcaatc											1533
cgccgattcc	ccggcccgtc	ccgtcgccgt	ccaaccgcag	tacaatctgc	tggcccgcgg											1593
ggattatgag	accggtatcc	gcccgggtcgt	ggacgagttc	ggtcccgcgg												1643

<210> 10

<211> 346

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 10

Met	Gly	Ala	Met	Arg	Ile	Ala	Thr	Leu	Thr	Ser	Gly	Gly	Asp	Cys	Pro
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Gly	Leu	Asn	Ala	Val	Ile	Arg	Gly	Ile	Val	Arg	Thr	Ala	Ser	Asn	Glu
			20					25					30		
Phe	Gly	Ser	Thr	Val	Val	Gly	Tyr	Gln	Asp	Gly	Trp	Glu	Gly	Leu	Leu

		35					40					45					
Ala	Asp	Arg	Arg	Val	Gln	Leu	Tyr	Asp	Asp	Glu	Asp	Ile	Asp	Arg	Ile		
	50					55					60						
Leu	Leu	Arg	Gly	Gly	Thr	Ile	Leu	Gly	Thr	Gly	Arg	Leu	His	Pro	Asp		
	65				70					75					80		
Lys	Phe	Arg	Ala	Gly	Ile	Asp	Gln	Val	Lys	Ala	Asn	Leu	Ala	Asp	Ala		
				85					90					95			
Gly	Ile	Asp	Ala	Leu	Ile	Pro	Ile	Gly	Gly	Glu	Gly	Thr	Leu	Lys	Gly		
			100					105				110					
Ala	Lys	Trp	Leu	Ala	Asp	Asn	Gly	Ile	Pro	Val	Val	Gly	Val	Pro	Lys		
		115					120					125					
Thr	Ile	Asp	Asn	Asp	Val	Asn	Gly	Thr	Asp	Phe	Thr	Phe	Gly	Phe	Asp		
	130					135					140						
Ser	Ala	Val	Ser	Val	Ala	Thr	Asp	Ala	Ile	Asp	Arg	Leu	His	Thr	Thr		
	145				150					155					160		
Ala	Glu	Ser	His	Asn	Arg	Val	Met	Ile	Val	Glu	Val	Met	Gly	Arg	His		
				165				170					175				
Val	Gly	Trp	Ile	Ala	Leu	His	Ala	Gly	Met	Ala	Gly	Gly	Ala	His	Tyr		
			180					185				190					
Thr	Val	Ile	Pro	Glu	Val	Pro	Phe	Asp	Ile	Ser	Glu	Ile	Cys	Lys	Arg		
		195					200					205					
Met	Glu	Arg	Arg	Phe	Gln	Met	Gly	Glu	Lys	Tyr	Gly	Ile	Ile	Val	Val		
	210				215						220						
Ala	Glu	Gly	Ala	Leu	Pro	Lys	Glu	Gly	Thr	Met	Glu	Leu	Arg	Glu	Gly		
	225				230					235					240		
Glu	Val	Asp	Gln	Phe	Gly	His	Lys	Thr	Phe	Thr	Gly	Ile	Gly	Gln	Gln		
				245					250					255			
Ile	Ala	Asp	Glu	Val	His	Arg	Arg	Leu	Gly	His	Asp	Val	Arg	Thr	Thr		
			260					265					270				
Val	Leu	Gly	His	Ile	Gln	Arg	Gly	Gly	Thr	Pro	Thr	Ala	Phe	Asp	Arg		
		275					280					285					
Val	Leu	Ala	Thr	Arg	Tyr	Gly	Val	Arg	Ala	Ala	Arg	Ala	Cys	His	Glu		
	290					295					300						
Gly	Gln	Phe	Asn	Thr	Val	Val	Ala	Leu	Lys	Gly	Glu	Arg	Ile	Arg	Met		
	305				310					315					320		
Ile	Ser	Phe	Asp	Glu	Ala	Val	Gly	Thr	Leu	Lys	Lys	Val	Pro	Met	Glu		
				325					330					335			
Arg	Trp	Val	Thr	Ala	Gln	Ala	Met	Phe	Gly								
			340					345									

<210> 11
 <211> 498
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>
 <221> CDS
 <222> (1)..(498)

<400> 11
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Tyr 1	Tyr	Gln	His	Asp 5	Pro	Gly	Phe	Pro	Phe 10	Ala	Pro	Lys	Arg	Thr 15	Gly	
tg	g	c	a	a	a	c	c	t	a	c	c	c	a	t	c	g
Trp	Ala	His	Thr	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gln	Arg	Leu	Gln	Trp	
			20					25					30			
ac	c	c	t	c	a	c	c	t	a	c	c	a	t	a	c	g
Thr	His	Leu	Pro	Asp	Ala	Leu	Tyr	Pro	Asp	Val	Ser	Tyr	Asp	Leu	Asp	
		35					40					45				
g	a	t	a	c	c	a	c	c	a	c	c	a	c	c	a	c
Gly	Cys	Tyr	Ser	Gly	Gly	Ala	Val	Phe	Ser	Asp	Gly	Thr	Leu	Lys	Leu	
	50					55				60						
t	t	a	c	a	c	a	a	a	a	c	c	c	c	a	a	a
Phe	Tyr	Thr	Gly	Asn	Arg	Lys	Ile	Asp	Gly	Lys	Arg	Arg	Ala	Thr	Gln	
65					70					75				80		
a	a	c	c	a	c	a	c	a	c	c	a	c	c	a	a	c
Asn	Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	Gly	Gly	Ile	His	
			85						90					95		
c	c	c	c	a	a	a	c	c	a	c	c	c	a	c	c	c
Arg	Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe	
			100					105					110			
a	c	c	c	a	c	a	c	a	c	c	a	c	c	a	c	c
Thr	Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp	
		115					120					125				
a	a	c	c	a	c	a	c	a	a	c	c	a	c	c	a	c
Lys	Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val	
	130					135				140						
c	t	a	c	c	a	a	c	a	a	c	t	c	c	c	a	a
Leu	Tyr	Arg	Ser	Ala	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu	Ile	
145					150					155					160	
a	c	c	c	a	c	a	c	a	c							
Thr	Phe	Asp	Leu	Ser	Asp											
				165												

<210> 12

<211> 166

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 12

Tyr 1	Tyr	Gln	His	Asp 5	Pro	Gly	Phe	Pro	Phe 10	Ala	Pro	Lys	Arg	Thr 15	Gly	
Trp	Ala	His	Thr	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gln	Arg	Leu	Gln	Trp	
			20					25					30			
Thr	His	Leu	Pro	Asp	Ala	Leu	Tyr	Pro	Asp	Val	Ser	Tyr	Asp	Leu	Asp	
		35					40					45				
Gly	Cys	Tyr	Ser	Gly	Gly	Ala	Val	Phe	Ser	Asp	Gly	Thr	Leu	Lys	Leu	
	50					55				60						
Phe	Tyr	Thr	Gly	Asn	Arg	Lys	Ile	Asp	Gly	Lys	Arg	Arg	Ala	Thr	Gln	
65					70					75				80		
Asn	Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	Gly	Gly	Ile	His	
				85					90					95		

Arg	Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe
			100					105					110		
Thr	Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp
		115					120					125			
Lys	Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val
	130					135					140				
Leu	Tyr	Arg	Ser	Ala	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu	Ile
145					150					155					160
Thr	Phe	Asp	Leu	Ser	Asp										
				165											

<210> 13

<211> 479

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(477)

<400> 13

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1				5				10						15		
tgg	gct	cac	acc	acc	acg	ccg	ttg	acc	gga	ccg	cag	cga	ttg	cag	tgg	96
Trp	Ala	His	Thr	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gln	Arg	Leu	Gln	Trp	
			20					25					30			
acg	cac	ctg	ccc	gac	gct	ctt	tac	ccg	gat	gca	tcc	tat	gac	ctg	gat	144
Thr	His	Leu	Pro	Asp	Ala	Leu	Tyr	Pro	Asp	Ala	Ser	Tyr	Asp	Leu	Asp	
		35				40						45				
gga	tgc	tat	tcc	ggt	gga	gcc	gta	ttt	act	gac	ggc	aca	ctt	aaa	ctt	192
Gly	Cys	Tyr	Ser	Gly	Gly	Ala	Val	Phe	Thr	Asp	Gly	Thr	Leu	Lys	Leu	
	50					55					60					
ttc	tac	acc	ggc	aac	cta	aaa	att	gac	ggc	aag	cgc	cgc	gcc	acc	caa	240
Phe	Tyr	Thr	Gly	Asn	Leu	Lys	Ile	Asp	Gly	Lys	Arg	Arg	Ala	Thr	Gln	
	65			70						75					80	
aac	ctc	gtc	gaa	gtc	gag	gac	cca	act	ggg	ctg	atg	ggc	ggc	att	cat	288
Asn	Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	Gly	Gly	Ile	His	
			85					90						95		
cgc	cgt	tcg	cct	aaa	aat	ccg	ctt	atc	gac	gga	ccc	gcc	agc	ggt	ttc	336
Arg	Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe	
			100					105					110			
aca	ccc	cat	tac	cgc	gat	ccc	atg	atc	agc	cct	gat	ggt	gat	ggt	tgg	384
Thr	Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp	
		115					120					125				
aaa	atg	ggt	ctt	ggg	gcc	caa	cgc	gaa	aac	ctc	acc	ggt	gca	gcg	gtt	432
Lys	Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val	
	130					135					140					
cta	tac	cgc	tcg	aca	gat	ctt	gaa	aac	tgg	gaa	ttc	tcc	ggt	gaa	at	479
Leu	Tyr	Arg	Ser	Thr	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu		
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<210> 14
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 <212> PRT
 <213> Corynebacterium thermoaminogenes

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 1 5 10 15
 Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
 20 25 30
 Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp
 35 40 45
 Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu
 50 55 60
 Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
 65 70 75 80
 Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
 85 90 95
 Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
 100 105 110
 Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
 115 120 125
 Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
 130 135 140
 Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu
 145 150 155

<210> 15
 <211> 490
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<400> 15
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 tttagaacct ggagatgaag aagaaaaatg gttgtttctc tggtagacagt atagtcaaag 180
 atgataagtt gtattttatct tatacagggt accattatta taatgacgat gatcccgatc 240
 atttttggca aaatcaaaat atggccttata gtgaagatgg cattcatttt caaaaatata 300
 aacaaaatgc aatcattcct accccacctg aagataatac acatcacttc agagatccaa 360
 aggtatggga acatccatgg cttattatta catgatagta ggtagtcaaa atgatagaga 420
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<210> 16
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 <213> Corynebacterium thermoaminogenes

<220>
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<222> (637)..(1362)

<220>

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<222> (1434)..(2315)

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<222> (3235)..(4065)

<400> 16

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cctcctcgag	cagaccggag	agacgctcgg	aatcgtggac	gttcatctgg	cagccgaagg	180										
tacgcacctc	ataggtgcgg	gcagtgggtg	cctccccggt	cccccgcgcc	gggaggggtg	240										
cggcggggtg	gtccgggtgg	gatggatggg	tgttcatctg	gtgggtatca	atctgctgcg	300										
tcacgggagg	taattgtatc	ggccgcgggc	accctgacat	aaacgtccga	tccagaggaa	360										
cgcaaccccc	tggagtgtcg	cagccatgca	ggttgggcaa	caccgtaacg	gaacctagca	420										
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gaaattcatt	tcaaaatgga	ctcaatcaca	ggatttacc	cacatgaccc	aacattcctt	600										
tatgctatcc	ccatgacgca	gaccacaaat	caccgcg	atg	atc aag atg acg ggg	654										
			Met	Ile Lys Met Thr Gly												
			1	5												
gtg	cag	aag	ttc	ttc	gat	gac	ttc	cag	gcc	ctg	acc	gat	atc	aat	ctt	702
Val	Gln	Lys	Phe	Phe	Asp	Asp	Phe	Gln	Ala	Leu	Thr	Asp	Ile	Asn	Leu	
			10					15					20			
gag	gtc	ccc	gcg	gga	cag	gtc	gtt	gtt	gtt	ctc	ggc	ccg	tcc	ggg	tcc	750
Glu	Val	Pro	Ala	Gly	Gln	Val	Val	Val	Val	Leu	Gly	Pro	Ser	Gly	Ser	
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gga	aag	tcg	acg	ctg	tgc	cgc	acc	atc	aac	cgc	ctc	gaa	acc	atc	gag	798
Gly	Lys	Ser	Thr	Leu	Cys	Arg	Thr	Ile	Asn	Arg	Leu	Glu	Thr	Ile	Glu	
		40				45					50					
gag	gga	acc	atc	gag	atc	gat	gga	aaa	ctg	ctt	ccg	gag	gag	ggc	aag	846
Glu	Gly	Thr	Ile	Glu	Ile	Asp	Gly	Lys	Leu	Leu	Pro	Glu	Glu	Gly	Lys	
		55			60					65					70	
gac	ctg	gcc	aag	atc	cgt	gcc	gac	gtg	ggc	atg	gtg	ttc	cag	tct	ttc	894
Asp	Leu	Ala	Lys	Ile	Arg	Ala	Asp	Val	Gly	Met	Val	Phe	Gln	Ser	Phe	
				75					80					85		
aac	ctc	ttc	ccc	cac	ctc	acc	atc	aag	gac	aat	gtc	acc	ctc	ggc	ccg	942
Asn	Leu	Phe	Pro	His	Leu	Thr	Ile	Lys	Asp	Asn	Val	Thr	Leu	Gly	Pro	
			90					95					100			
atg	aag	gtc	cgg	aag	atg	aag	aag	tcc	gag	gcc	aat	gag	gtg	gcc	atg	990
Met	Lys	Val	Arg	Lys	Met	Lys	Lys	Ser	Glu	Ala	Asn	Glu	Val	Ala	Met	
		105					110					115				
aag	ctg	ttg	gaa	cgc	gtc	ggc	atc	gcc	aac	cag	gcc	gag	aaa	tac	ccg	1038
Lys	Leu	Leu	Glu	Arg	Val	Gly	Ile	Ala	Asn	Gln	Ala	Glu	Lys	Tyr	Pro	

120	125	130	
gca cag ctc tcg ggc ggg	cag cag cag cgc	gtg gcc atc gcc cgc gca	1086
Ala Gln Leu Ser Gly Gly	Gln Gln Gln Arg	Val Ala Ile Ala Arg Ala	
135	140	145	150
ctg gcg atg aac ccc aag	atc atg ctt ttc	gac gaa cca acc tcc gcc	1134
Leu Ala Met Asn Pro Lys	Ile Met Leu Phe	Asp Glu Pro Thr Ser Ala	
	155	160	165
ctc gac ccc gag atg gtc	aac gag gtt ctg	gac gtc atg gcg agt ctg	1182
Leu Asp Pro Glu Met Val	Asn Glu Val Leu	Asp Val Met Ala Ser Leu	
	170	175	180
gcc aag gaa ggc atg acc	atg gtg tgt gtc	acc cac gag atg ggt ttc	1230
Ala Lys Glu Gly Met Thr	Met Val Cys Val	Thr His Glu Met Gly Phe	
	185	190	195
gca cgc agg gcc gca gac	cgt gtg ctg ttc	atg tct gac ggc gcc atc	1278
Ala Arg Arg Ala Ala Asp	Arg Val Leu Phe	Met Ser Asp Gly Ala Ile	
	200	205	210
gtc gag gac tcc gac ccg	gag acc ttc ttc	acc aat cca caa acc gac	1326
Val Glu Asp Ser Asp Pro	Glu Thr Phe Phe	Thr Asn Pro Gln Thr Asp	
	215	220	225
cgg gcg aag gat ttc ctg	ggc aag atc ctc	gcc cac tgacctcccc	1372
Arg Ala Lys Asp Phe Leu	Gly Lys Ile Leu	Ala His	
	235	240	
tcactctgtg tccaactccc	ccgctggcca aaatcagcga	ccatgaccaa caggagcatc	1432
a atg tcg cac aaa cgc	atg ttc acc cgt ctc	gcc gca gcc acc agc gca	1481
Met Ser His Lys Arg Met	Phe Thr Arg Leu Ala	Ala Ala Thr Ser Ala	
	245	250	255
gct gtt ctc gcc ggc atc	acc ctc acc gcc	tgt ggt gat tcc gag ggt	1529
Ala Val Leu Ala Gly Ile	Thr Leu Thr Ala	Cys Gly Asp Ser Glu Gly	
	260	265	270
ggt gac ggt ctg ctc gcc	gcc atc gaa aat	ggc aat gtc acc atc ggc	1577
Gly Asp Gly Leu Leu Ala	Ala Ile Glu Asn	Gly Asn Val Thr Ile Gly	
	275	280	285
acc aag tac gat cag ccg	ggt ctg gga ctg	cgt aac ccg gac aat tcc	1625
Thr Lys Tyr Asp Gln Pro	Gly Leu Gly Leu	Arg Asn Pro Asp Asn Ser	
	295	300	305
atg agc gga ctg gat gtc	gac gtc gcg cag	tac gtg gtc aac tcc atc	1673
Met Ser Gly Leu Asp Val	Asp Val Ala Gln	Tyr Val Val Asn Ser Ile	
	310	315	320
gcc gat gac aac ggt tgg	gat cac ccc acc	gtg gaa tgg cgc gag acc	1721
Ala Asp Asp Asn Gly Trp	Asp His Pro Thr	Val Glu Trp Arg Glu Thr	
	325	330	335
ccc tcc gcc cag cgc gag	acc ctc atc cag	aac ggt gag gtg gat atg	1769
Pro Ser Ala Gln Arg Glu	Thr Leu Ile Gln	Asn Gly Glu Val Asp Met	
	340	345	350
atc gcc gca acc tac tcc	atc aac ccc gga	cgc tcc gaa tcg gtg aac	1817
Ile Ala Ala Thr Tyr Ser	Ile Asn Pro Gly	Arg Ser Glu Ser Val Asn	
	355	360	365
ttc ggt gga cca tac ctc	ctc acc cac cag	gcc ctc ctg gtc cgc gag	1865
Phe Gly Gly Pro Tyr Leu	Leu Leu Thr His	Gln Ala Leu Leu Val Arg Glu	
	375	380	385
gac gat gac cgc atc cag	acc ctc gag gac	ctc gat gac ggc ctg atc	1913

Asp	Asp	Asp	Arg	Ile	Gln	Thr	Leu	Glu	Asp	Leu	Asp	Asp	Gly	Leu	Ile	
			390					395					400			
ctg	tgt	tcc	gtt	acc	gga	tcc	acc	ccc	gcc	cag	aag	gtc	aag	gat	gtc	1961
Leu	Cys	Ser	Val	Thr	Gly	Ser	Thr	Pro	Ala	Gln	Lys	Val	Lys	Asp	Val	
		405					410					415				
ctc	ccc	ggc	gtc	cag	ctg	cag	gaa	tac	gac	acc	tac	tcc	tcc	tgt	gtg	2009
Leu	Pro	Gly	Val	Gln	Leu	Gln	Glu	Tyr	Asp	Thr	Tyr	Ser	Ser	Cys	Val	
	420					425					430					
gag	gca	ctg	agc	cag	ggc	aac	gtc	gat	gca	atg	acc	acc	gac	gcc	acc	2057
Glu	Ala	Leu	Ser	Gln	Gly	Asn	Val	Asp	Ala	Met	Thr	Thr	Asp	Ala	Thr	
435					440					445					450	
atc	ctc	ttc	ggc	tac	gcg	cag	cag	cgc	gaa	ggg	gaa	ttc	cgc	gtc	gtg	2105
Ile	Leu	Phe	Gly	Tyr	Ala	Gln	Gln	Arg	Glu	Gly	Glu	Phe	Arg	Val	Val	
			455					460						465		
gag	atg	gaa	cag	gac	ggc	gag	ccg	ttc	acc	aat	gag	tac	tac	ggc	atc	2153
Glu	Met	Glu	Gln	Asp	Gly	Glu	Pro	Phe	Thr	Asn	Glu	Tyr	Tyr	Gly	Ile	
			470				475						480			
ggg	atc	acc	aag	gat	gac	acc	gaa	gcc	acc	gat	gcg	atc	aac	gca	gcg	2201
Gly	Ile	Thr	Lys	Asp	Asp	Thr	Glu	Ala	Thr	Asp	Ala	Ile	Asn	Ala	Ala	
		485				490						495				
ttg	gag	cgt	atg	tac	gcc	gac	ggg	tcc	ttc	cag	cgt	ttc	ctc	acc	gag	2249
Leu	Glu	Arg	Met	Tyr	Ala	Asp	Gly	Ser	Phe	Gln	Arg	Phe	Leu	Thr	Glu	
	500					505					510					
aac	ctc	ggc	gag	gat	tcc	cag	gtt	gtc	cag	gag	ggc	acc	ccg	ggg	gac	2297
Asn	Leu	Gly	Glu	Asp	Ser	Gln	Val	Val	Gln	Glu	Gly	Thr	Pro	Gly	Asp	
515					520					525					530	
ctc	tcc	ttc	ctg	gac	gag	tgacctgacg	gggcccgaacg	cccgatgagc								2345
Leu	Ser	Phe	Leu	Asp	Glu											
			535													
atgcgtggcc	cccgcatccc	gggggtgccac	gcacatcac	tttcaccact	gatcccctac											2405
cgttccttac	cgaggagaaa	ttcccc	atg agt aca tta tgg gcg gat ctg ggt													2458
			Met Ser Thr Leu Trp Ala Asp Leu Gly													
			540												545	
ccg	tca	ctc	cta	ccc	gca	ttc	tgg	gtg	aca	atc	caa	ctc	acc	gtc	tat	2506
Pro	Ser	Leu	Leu	Pro	Ala	Phe	Trp	Val	Thr	Ile	Gln	Leu	Thr	Val	Tyr	
			550						555					560		
tcc	gcc	atc	gga	tcc	atg	atc	ctc	ggg	acc	atc	ctc	acc	gcc	atg	agg	2554
Ser	Ala	Ile	Gly	Ser	Met	Ile	Leu	Gly	Thr	Ile	Leu	Thr	Ala	Met	Arg	
			565					570					575			
gtg	tcc	ccg	gtg	aag	atc	ctg	cg	agc	ata	tcc	acc	gcc	tac	atc	aac	2602
Val	Ser	Pro	Val	Lys	Ile	Leu	Arg	Ser	Ile	Ser	Thr	Ala	Tyr	Ile	Asn	
		580					585					590				
acg	gtc	cgt	aac	acc	cca	ctg	acc	ctg	gtg	atc	ctg	ttc	tgt	tcc	ttc	2650
Thr	Val	Arg	Asn	Thr	Pro	Leu	Thr	Leu	Val	Ile	Leu	Phe	Cys	Ser	Phe	
	595					600					605					
ggc	ctg	tat	cag	aac	ctc	ggg	ctc	acc	ctc	gcc	ggg	cg	gac	agt	tcc	2698
Gly	Leu	Tyr	Gln	Asn	Leu	Gly	Leu	Thr	Leu	Ala	Gly	Arg	Asp	Ser	Ser	
610					615					620					625	
acc	ttt	ctg	gcc	gat	aac	aac	ttc	cg	ctc	gcg	gtg	ctc	gga	ttc	atc	2746
Thr	Phe	Leu	Ala	Asp	Asn	Asn	Phe	Arg	Leu	Ala	Val	Leu	Gly	Phe	Ile	
			630					635						640		

ctg	tac	acc	tcc	gcc	ttc	gtt	gcg	gaa	tca	ctc	cgg	tca	ggc	atc	aac	2794
Leu	Tyr	Thr	Ser	Ala	Phe	Val	Ala	Glu	Ser	Leu	Arg	Ser	Gly	Ile	Asn	
			645					650					655			
acc	gtg	cac	ttc	ggg	cag	gcg	gag	gcc	gcc	cgg	tcg	ctg	gga	ctc	ggt	2842
Thr	Val	His	Phe	Gly	Gln	Ala	Glu	Ala	Ala	Arg	Ser	Leu	Gly	Leu	Gly	
		660					665					670				
ttc	agt	gac	atc	ttc	cgg	tcc	atc	atc	ttc	ccc	cag	gcg	gtg	cgt	gcc	2890
Phe	Ser	Asp	Ile	Phe	Arg	Ser	Ile	Ile	Phe	Pro	Gln	Ala	Val	Arg	Ala	
	675					680					685					
gcc	atc	atc	ccg	ctg	ggc	aac	acc	ctc	atc	gcc	ctg	acc	aag	aac	acc	2938
Ala	Ile	Ile	Pro	Leu	Gly	Asn	Thr	Leu	Ile	Ala	Leu	Thr	Lys	Asn	Thr	
690					695					700					705	
acg	atc	gcg	tcc	gtg	atc	ggc	gtc	ggt	gag	gcc	tcg	ctg	ctg	atg	aag	2986
Thr	Ile	Ala	Ser	Val	Ile	Gly	Val	Gly	Glu	Ala	Ser	Leu	Leu	Met	Lys	
			710					715						720		
tcc	acg	att	gaa	aat	cat	gcc	aac	atg	ctc	ttc	gtc	gtg	ttc	gcc	atc	3034
Ser	Thr	Ile	Glu	Asn	His	Ala	Asn	Met	Leu	Phe	Val	Val	Phe	Ala	Ile	
			725				730						735			
ttc	gcc	gtc	ggc	ttc	atg	atc	ctc	acc	ctc	ccc	atg	ggc	ctg	ggg	ctt	3082
Phe	Ala	Val	Gly	Phe	Met	Ile	Leu	Thr	Leu	Pro	Met	Gly	Leu	Gly	Leu	
		740					745					750				
gga	aaa	ctc	gct	gag	aaa	atg	gcg	gtg	aag	aaa	taatgtcctc ctccgtacgc				3135	
Gly	Lys	Leu	Ala	Glu	Lys	Met	Ala	Val	Lys	Lys						
	755					760										
gcaacagtcc tctacgacgc ccccgggcccc cggggacgca ggtccaacac catcatcacc																3195
atcgccacca ccctggtggc agtggccgctc ctgttctgg gtg ggc agt gtt ctc																3249
											Val	Gly	Ser	Val	Leu	
											765					
cag	gaa	aac	ggc	cag	ttg	gac	ggc	gac	aaa	tgg	acc	ccg	ttc	ctc	gat	3297
Gln	Glu	Asn	Gly	Gln	Leu	Asp	Gly	Asp	Lys	Trp	Thr	Pro	Phe	Leu	Asp	
770					775					780					785	
ccc	cag	acc	tgg	acc	acc	tat	ctt	ctg	ccc	ggc	ctg	tgg	gga	acc	ctg	3345
Pro	Gln	Thr	Trp	Thr	Thr	Tyr	Leu	Leu	Pro	Gly	Leu	Trp	Gly	Thr	Leu	
			790						795					800		
aag	gca	gcg	gtg	gcc	tcc	atc	ctt	ctc	gcg	ctg	atc	atg	ggc	acc	ctg	3393
Lys	Ala	Ala	Val	Ala	Ser	Ile	Leu	Leu	Ala	Leu	Ile	Met	Gly	Thr	Leu	
			805					810					815			
ctc	ggg	ctc	gga	cgc	atc	tcc	gaa	atc	cgg	ctc	ctg	cgc	tgg	ttc	tgc	3441
Leu	Gly	Leu	Gly	Arg	Ile	Ser	Glu	Ile	Arg	Leu	Leu	Arg	Trp	Phe	Cys	
		820					825					830				
ggg	atc	atc	atc	gag	acc	ttc	cgt	gcc	atc	ccg	gtg	ctg	atc	ctc	atg	3489
Gly	Ile	Ile	Ile	Glu	Thr	Phe	Arg	Ala	Ile	Pro	Val	Leu	Ile	Leu	Met	
	835					840					845					
atc	ttc	gcc	tat	cag	ttg	ttc	gcc	cgt	tac	cag	ctc	gtt	cca	tca	cgc	3537
Ile	Phe	Ala	Tyr	Gln	Leu	Phe	Ala	Arg	Tyr	Gln	Leu	Val	Pro	Ser	Arg	
					855					860					865	
cag	ctg	gcc	ttc	gcc	gcg	gtg	gtc	ttc	ggt	ctc	acc	atg	tac	aac	ggc	3585
Gln	Leu	Ala	Phe	Ala	Ala	Val	Val	Phe	Gly	Leu	Thr	Met	Tyr	Asn	Gly	
			870					875						880		
tcc	gtc	atc	gcc	gag	atc	ctt	aga	tcg	ggt	atc	gcc	tcc	ctg	ccg	aag	3633
Ser	Val	Ile	Ala	Glu	Ile	Leu	Arg	Ser	Gly	Ile	Ala	Ser	Leu	Pro	Lys	

	885		890		895		
gga cag cgt gag gcg gcg atc gcc ctg ggc atg tca acc cgc cag acc							3681
Gly Gln Arg Glu Ala Ala Ile Ala Leu Gly Met Ser Thr Arg Gln Thr							
	900		905		910		
acc tgg tcg atc ctg ctc ccc cag gcg gtg gca gcg atg ctg ccc gcc							3729
Thr Trp Ser Ile Leu Leu Pro Gln Ala Val Ala Ala Met Leu Pro Ala							
	915		920		925		
ctg atc gcg cag atg gtc atc gcg ctg aag gac tcc gcc ctc ggt tac							3777
Leu Ile Ala Gln Met Val Ile Ala Leu Lys Asp Ser Ala Leu Gly Tyr							
	930		935		940		945
cag atc ggt tat atc gag gtg gta cgc tcc ggt atc cag tcc gca tcc							3825
Gln Ile Gly Tyr Ile Glu Val Val Arg Ser Gly Ile Gln Ser Ala Ser							
	950		955		960		
gtc aac cgg aac tac ctg gct gcc ctc gcg gtg gtc gcg gtc atc atg							3873
Val Asn Arg Asn Tyr Leu Ala Ala Leu Ala Val Val Ala Val Ile Met							
	965		970		975		
atc ctg atc aac ttc gca ctg acc gca ctg gca gag cgt atc cag cgt							3921
Ile Leu Ile Asn Phe Ala Leu Thr Ala Leu Ala Glu Arg Ile Gln Arg							
	980		985		990		
cag ctg cgt gcc gga cgt gcc cgc agg aac att gtg gca aag gtg ccc							3969
Gln Leu Arg Ala Gly Arg Ala Arg Arg Asn Ile Val Ala Lys Val Pro							
	995		1000		1005		
gag gaa ccc gat cag ggc ctg gat acc aag gac aat gtg aac gtg gat							4017
Glu Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp Asn Val Asn Val Asp							
	1010		1015		1020		1025
tgg cac gat ccc gat tac aag gaa gtc aaa cac ccg gga ccg tca ttc							4065
Trp His Asp Pro Asp Tyr Lys Glu Val Lys His Pro Gly Pro Ser Phe							
	1030		1035		1040		
tgacaggtcc ctggatcccc gctgcggtca ggaggcgggt gcaacaatga agtccggctg							4125
cccagatgtc tggggcagcc ggactttgtg gcagatcaat gctgactgag gtcctcgatg							4185
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<210> 17

<211> 242

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 17

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Leu Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn	
35 40 45	
Arg Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu	
50 55 60	
Leu Pro Glu Glu Gly Lys Asp Leu Ala Lys Ile Arg Ala Asp Val Gly	
65 70 75 80	
Met Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp	
85 90 95	

Asn	Val	Thr	Leu	Gly	Pro	Met	Lys	Val	Arg	Lys	Met	Lys	Lys	Ser	Glu
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Ala	Asn	Glu	Val	Ala	Met	Lys	Leu	Leu	Glu	Arg	Val	Gly	Ile	Ala	Asn
		115					120					125			
Gln	Ala	Glu	Lys	Tyr	Pro	Ala	Gln	Leu	Ser	Gly	Gly	Gln	Gln	Gln	Arg
		130				135					140				
Val	Ala	Ile	Ala	Arg	Ala	Leu	Ala	Met	Asn	Pro	Lys	Ile	Met	Leu	Phe
145					150					155					160
Asp	Glu	Pro	Thr	Ser	Ala	Leu	Asp	Pro	Glu	Met	Val	Asn	Glu	Val	Leu
				165					170					175	
Asp	Val	Met	Ala	Ser	Leu	Ala	Lys	Glu	Gly	Met	Thr	Met	Val	Cys	Val
			180					185					190		
Thr	His	Glu	Met	Gly	Phe	Ala	Arg	Arg	Ala	Ala	Asp	Arg	Val	Leu	Phe
		195					200					205			
Met	Ser	Asp	Gly	Ala	Ile	Val	Glu	Asp	Ser	Asp	Pro	Glu	Thr	Phe	Phe
		210				215					220				
Thr	Asn	Pro	Gln	Thr	Asp	Arg	Ala	Lys	Asp	Phe	Leu	Gly	Lys	Ile	Leu
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<210> 18

<211> 294

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 18

Met	Ser	His	Lys	Arg	Met	Phe	Thr	Arg	Leu	Ala	Ala	Ala	Thr	Ser	Ala
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Ala	Val	Leu	Ala	Gly	Ile	Thr	Leu	Thr	Ala	Cys	Gly	Asp	Ser	Glu	Gly
			20					25					30		
Gly	Asp	Gly	Leu	Leu	Ala	Ala	Ile	Glu	Asn	Gly	Asn	Val	Thr	Ile	Gly
		35					40					45			
Thr	Lys	Tyr	Asp	Gln	Pro	Gly	Leu	Gly	Leu	Arg	Asn	Pro	Asp	Asn	Ser
	50					55					60				
Met	Ser	Gly	Leu	Asp	Val	Asp	Val	Ala	Gln	Tyr	Val	Val	Asn	Ser	Ile
65					70				75						80
Ala	Asp	Asp	Asn	Gly	Trp	Asp	His	Pro	Thr	Val	Glu	Trp	Arg	Glu	Thr
				85					90					95	
Pro	Ser	Ala	Gln	Arg	Glu	Thr	Leu	Ile	Gln	Asn	Gly	Glu	Val	Asp	Met
			100					105					110		
Ile	Ala	Ala	Thr	Tyr	Ser	Ile	Asn	Pro	Gly	Arg	Ser	Glu	Ser	Val	Asn
		115					120					125			
Phe	Gly	Gly	Pro	Tyr	Leu	Leu	Thr	His	Gln	Ala	Leu	Leu	Val	Arg	Glu
	130					135					140				
Asp	Asp	Asp	Arg	Ile	Gln	Thr	Leu	Glu	Asp	Leu	Asp	Asp	Gly	Leu	Ile
145					150					155					160
Leu	Cys	Ser	Val	Thr	Gly	Ser	Thr	Pro	Ala	Gln	Lys	Val	Lys	Asp	Val
				165					170					175	
Leu	Pro	Gly	Val	Gln	Leu	Gln	Glu	Tyr	Asp	Thr	Tyr	Ser	Ser	Cys	Val
			180					185					190		
Glu	Ala	Leu	Ser	Gln	Gly	Asn	Val	Asp	Ala	Met	Thr	Thr	Asp	Ala	Thr

Ile	Leu	Phe	Gly	Tyr	Ala	Gln	Gln	Arg	Glu	Gly	Glu	Phe	Arg	Val	Val
	210					215					220				
Glu	Met	Glu	Gln	Asp	Gly	Glu	Pro	Phe	Thr	Asn	Glu	Tyr	Tyr	Gly	Ile
225					230					235					240
Gly	Ile	Thr	Lys	Asp	Asp	Thr	Glu	Ala	Thr	Asp	Ala	Ile	Asn	Ala	Ala
				245					250					255	
Leu	Glu	Arg	Met	Tyr	Ala	Asp	Gly	Ser	Phe	Gln	Arg	Phe	Leu	Thr	Glu
			260					265					270		
Asn	Leu	Gly	Glu	Asp	Ser	Gln	Val	Val	Gln	Glu	Gly	Thr	Pro	Gly	Asp
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Leu	Ser	Phe	Leu	Asp	Glu										
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<210> 19

<211> 228

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 19

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			20					25					30		
Leu	Gly	Thr	Ile	Leu	Thr	Ala	Met	Arg	Val	Ser	Pro	Val	Lys	Ile	Leu
		35					40					45			
Arg	Ser	Ile	Ser	Thr	Ala	Tyr	Ile	Asn	Thr	Val	Arg	Asn	Thr	Pro	Leu
	50					55					60				
Thr	Leu	Val	Ile	Leu	Phe	Cys	Ser	Phe	Gly	Leu	Tyr	Gln	Asn	Leu	Gly
65					70					75					80
Leu	Thr	Leu	Ala	Gly	Arg	Asp	Ser	Ser	Thr	Phe	Leu	Ala	Asp	Asn	Asn
				85					90					95	
Phe	Arg	Leu	Ala	Val	Leu	Gly	Phe	Ile	Leu	Tyr	Thr	Ser	Ala	Phe	Val
			100					105					110		
Ala	Glu	Ser	Leu	Arg	Ser	Gly	Ile	Asn	Thr	Val	His	Phe	Gly	Gln	Ala
		115					120					125			
Glu	Ala	Ala	Arg	Ser	Leu	Gly	Leu	Gly	Phe	Ser	Asp	Ile	Phe	Arg	Ser
	130					135					140				
Ile	Ile	Phe	Pro	Gln	Ala	Val	Arg	Ala	Ala	Ile	Ile	Pro	Leu	Gly	Asn
145					150					155					160
Thr	Leu	Ile	Ala	Leu	Thr	Lys	Asn	Thr	Thr	Ile	Ala	Ser	Val	Ile	Gly
				165					170					175	
Val	Gly	Glu	Ala	Ser	Leu	Leu	Met	Lys	Ser	Thr	Ile	Glu	Asn	His	Ala
			180					185					190		
Asn	Met	Leu	Phe	Val	Val	Phe	Ala	Ile	Phe	Ala	Val	Gly	Phe	Met	Ile
		195					200					205			
Leu	Thr	Leu	Pro	Met	Gly	Leu	Gly	Leu	Gly	Lys	Leu	Ala	Glu	Lys	Met
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Ala	Val	Lys	Lys												
225															

<210> 20
 <211> 277
 <212> PRT
 <213> Corynebacterium thermoaminogenes

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 35 40 45
 Ile Met Gly Thr Leu Leu Gly Leu Gly Arg Ile Ser Glu Ile Arg Leu
 50 55 60
 Leu Arg Trp Phe Cys Gly Ile Ile Ile Glu Thr Phe Arg Ala Ile Pro
 65 70 75 80
 Val Leu Ile Leu Met Ile Phe Ala Tyr Gln Leu Phe Ala Arg Tyr Gln
 85 90 95
 Leu Val Pro Ser Arg Gln Leu Ala Phe Ala Ala Val Val Phe Gly Leu
 100 105 110
 Thr Met Tyr Asn Gly Ser Val Ile Ala Glu Ile Leu Arg Ser Gly Ile
 115 120 125
 Ala Ser Leu Pro Lys Gly Gln Arg Glu Ala Ala Ile Ala Leu Gly Met
 130 135 140
 Ser Thr Arg Gln Thr Thr Trp Ser Ile Leu Leu Pro Gln Ala Val Ala
 145 150 155 160
 Ala Met Leu Pro Ala Leu Ile Ala Gln Met Val Ile Ala Leu Lys Asp
 165 170 175
 Ser Ala Leu Gly Tyr Gln Ile Gly Tyr Ile Glu Val Val Arg Ser Gly
 180 185 190
 Ile Gln Ser Ala Ser Val Asn Arg Asn Tyr Leu Ala Ala Leu Ala Val
 195 200 205
 Val Ala Val Ile Met Ile Leu Ile Asn Phe Ala Leu Thr Ala Leu Ala
 210 215 220
 Glu Arg Ile Gln Arg Gln Leu Arg Ala Gly Arg Ala Arg Arg Asn Ile
 225 230 235 240
 Val Ala Lys Val Pro Glu Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp
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 Asn Val Asn Val Asp Trp His Asp Pro Asp Tyr Lys Glu Val Lys His
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 Pro Gly Pro Ser Phe
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<210> 21
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<220>
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<400> 21

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ccgggcacgt tttcagctgc gggatgatga agcggtcgcc ggtcccccg tgcataaac 420
gaaatgaaaa acattccaac aggaggtgtg gaa atg gcc gat caa gca aaa ctt 474
                                Met Ala Asp Gln Ala Lys Leu
                                1                               5

ggt ggc aaa ccc aca gat gac acc aac ttc gcg atg atc cgt gat ggc 522
Gly Gly Lys Pro Thr Asp Asp Thr Asn Phe Ala Met Ile Arg Asp Gly
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Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Lys Glu Trp
                                25                               30                               35

atg gac tcc cta gac ggt cta ctg cag gat tcc tct ccg gag cgc gcc 618
Met Asp Ser Leu Asp Gly Leu Leu Gln Asp Ser Ser Pro Glu Arg Ala
                                40                               45                               50                               55

cgt tac ctg atg ctg cgc ctg ctg gag cgg gca tcc gcc aag cgt gtc 666
Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys Arg Val
                                60                               65                               70

cca ctg ccc ccg atg acg tcc acc gat tac gtc aac acc atc ccc aca 714
Pro Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile Pro Thr
                                75                               80                               85

tcc atg gag ccc gat ttc ccg ggt gat gag gag atg gag aag cgc tac 762
Ser Met Glu Pro Asp Phe Pro Gly Asp Glu Glu Met Glu Lys Arg Tyr
                                90                               95                               100

cgc cgc tgg atg cgc tgg aac gcc gcc atc atg gtg cac cgt gcc cag 810
Arg Arg Trp Met Arg Trp Asn Ala Ala Ile Met Val His Arg Ala Gln
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cgc ccg gga atc ggt gtg ggt ggg cac atc tcc acc tac gcc ggc gcc 858
Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala Gly Ala
                                120                               125                               130                               135

gcc cca ctc tac gag gtc ggt ttc aac cac ttc ttc cgc ggc aag gac 906
Ala Pro Leu Tyr Glu Val Gly Phe Asn His Phe Phe Arg Gly Lys Asp
                                140                               145                               150

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His Pro Gly Gly Gly Asp Gln Val Phe Phe Gln Gly His Ala Ser Pro
                                155                               160                               165

ggc atg tac gcc cgc gcc ttc ctc gag ggc cgt ctc acc gag agc gat 1002
Gly Met Tyr Ala Arg Ala Phe Leu Glu Gly Arg Leu Thr Glu Ser Asp
                                170                               175                               180

ctg gac agc ttc cgc cag gag gtc tcc tac gaa ggt ggt ggc atc ccg 1050
Leu Asp Ser Phe Arg Gln Glu Val Ser Tyr Glu Gly Gly Gly Ile Pro
                                185                               190                               195

tcc tac ccg cac ccg cac ggc atg ccg gac ttc tgg gag ttc ccg acc 1098
Ser Tyr Pro His Pro His Gly Met Pro Asp Phe Trp Glu Phe Pro Thr
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aac	cgc	tac	ctg	cac	aac	cgt	ggc	atc	aag	gac	acc	tcg	gag	cag	cac	1194
Asn	Arg	Tyr	Leu	His	Asn	Arg	Gly	Ile	Lys	Asp	Thr	Ser	Glu	Gln	His	
			235					240					245			
gtc	tgg	gca	ttc	ctc	ggt	gac	ggc	gag	atg	gat	gag	ccg	gag	tcc	cgt	1242
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Gly	Leu	Ile	His	Gln	Ala	Ala	Leu	Asn	Asn	Leu	Asp	Asn	Leu	Thr	Phe	
	265					270					275					
gtg	atc	aac	tgc	aac	ctg	cag	cgt	ctt	gat	ggc	ccg	gtc	cgc	ggt	aac	1338
Val	Ile	Asn	Cys	Asn	Leu	Gln	Arg	Leu	Asp	Gly	Pro	Val	Arg	Gly	Asn	
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Thr	Lys	Ile	Ile	Gln	Glu	Leu	Glu	Ser	Phe	Phe	Arg	Gly	Ala	Gly	Trp	
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tcc	gtc	atc	aag	gtc	atc	tgg	ggc	cgt	gag	tgg	gat	gaa	ctg	ctg	gag	1434
Ser	Val	Ile	Lys	Val	Ile	Trp	Gly	Arg	Glu	Trp	Asp	Glu	Leu	Leu	Glu	
			315					320					325			
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Lys	Asp	Gln	Asp	Gly	Ala	Leu	Val	Glu	Val	Met	Asn	Asn	Thr	Ser	Asp	
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ggt	gac	tac	cag	acc	ttc	aag	gcc	aat	gac	ggt	gcc	tac	gtc	cgt	gag	1530
Gly	Asp	Tyr	Gln	Thr	Phe	Lys	Ala	Asn	Asp	Gly	Ala	Tyr	Val	Arg	Glu	
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cac	ttc	ttc	ggc	cgt	gac	ccc	cgc	acc	ctc	aag	ctc	gtc	gag	gac	atg	1578
His	Phe	Phe	Gly	Arg	Asp	Pro	Arg	Thr	Leu	Lys	Leu	Val	Glu	Asp	Met	
360				365						370					375	
acc	gac	gag	gag	atc	tgg	aag	ctg	ccc	cgt	ggt	ggc	cat	gac	tac	cgt	1626
Thr	Asp	Glu	Glu	Ile	Trp	Lys	Leu	Pro	Arg	Gly	Gly	His	Asp	Tyr	Arg	
				380					385					390		
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Lys	Val	Tyr	Ala	Ala	Tyr	Lys	Arg	Ala	Leu	Glu	Thr	Lys	Asp	Arg	Pro	
			395					400					405			
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Thr	Val	Ile	Leu	Ala	His	Thr	Ile	Lys	Gly	Tyr	Gly	Leu	Gly	His	Asn	
		410					415					420				
ttc	gag	ggc	cgc	aac	gcg	acc	cac	cag	atg	aag	aag	ctg	acc	ctg	gat	1770
Phe	Glu	Gly	Arg	Asn	Ala	Thr	His	Gln	Met	Lys	Lys	Leu	Thr	Leu	Asp	
	425					430					435					
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Asp	Leu	Lys	Leu	Phe	Arg	Asp	Lys	Gln	Gly	Leu	Pro	Ile	Thr	Asp	Glu	
440				445						450					455	
gag	ctg	gag	aag	gat	ccc	tac	ctg	cct	ccg	tac	tac	cac	ccg	ggt	gag	1866
Glu	Leu	Glu	Lys	Asp	Pro	Tyr	Leu	Pro	Pro	Tyr	Tyr	His	Pro	Gly	Glu	
				460					465					470		
gac	gca	ccg	gag	atc	aag	tac	atg	aag	gag	cgt	cgc	cag	gcg	ctc	ggt	1914
Asp	Ala	Pro	Glu	Ile	Lys	Tyr	Met	Lys	Glu	Arg	Arg	Gln	Ala	Leu	Gly	
			475					480					485			

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Gly	Phe	Leu	Pro	Glu	Arg	Arg	Glu	Lys	Tyr	Glu	Pro	Leu	Gln	Val	Pro	
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ccg	ctg	gac	aag	ctg	cgg	tcc	gtg	cgc	aag	ggt	tcc	ggc	aag	cag	cag	2010
Pro	Leu	Asp	Lys	Leu	Arg	Ser	Val	Arg	Lys	Gly	Ser	Gly	Lys	Gln	Gln	
	505					510					515					
gtg	gcc	acc	acc	atg	gcc	acg	gtg	cgt	acc	ttc	aag	gaa	ctc	atg	cgg	2058
Val	Ala	Thr	Thr	Met	Ala	Thr	Val	Arg	Thr	Phe	Lys	Glu	Leu	Met	Arg	
	520				525					530					535	
gac	aag	aac	ctg	gcc	gac	cgc	ttg	gtc	ccg	atc	atc	ccg	gat	gag	gcc	2106
Asp	Lys	Asn	Leu	Ala	Asp	Arg	Leu	Val	Pro	Ile	Ile	Pro	Asp	Glu	Ala	
				540					545					550		
cgc	acc	ttc	ggc	ctg	gac	tcc	tgg	ttc	ccg	acc	ctg	aaa	atc	tac	aac	2154
Arg	Thr	Phe	Gly	Leu	Asp	Ser	Trp	Phe	Pro	Thr	Leu	Lys	Ile	Tyr	Asn	
			555					560					565			
ccg	cac	ggt	cag	aac	tac	gtg	ccg	gtc	gac	cat	gac	ctc	atg	ctg	tcc	2202
Pro	His	Gly	Gln	Asn	Tyr	Val	Pro	Val	Asp	His	Asp	Leu	Met	Leu	Ser	
		570					575					580				
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Tyr	Arg	Glu	Ala	Lys	Asp	Gly	Gln	Ile	Leu	His	Glu	Gly	Ile	Asn	Glu	
	585					590					595					
gcc	ggt	tcc	gtg	gca	tcg	ttt	atc	gcc	gcc	gga	acc	tcc	tac	gcc	acc	2298
Ala	Gly	Ser	Val	Ala	Ser	Phe	Ile	Ala	Ala	Gly	Thr	Ser	Tyr	Ala	Thr	
	600				605					610					615	
cat	ggc	gag	gcc	atg	atc	ccg	ctg	tac	atc	ttc	tac	tcg	atg	ttc	ggc	2346
His	Gly	Glu	Ala	Met	Ile	Pro	Leu	Tyr	Ile	Phe	Tyr	Ser	Met	Phe	Gly	
				620					625					630		
ttc	cag	cgc	acc	ggt	gac	ggc	atc	tgg	gcc	gca	gcc	gac	cag	atg	acg	2394
Phe	Gln	Arg	Thr	Gly	Asp	Gly	Ile	Trp	Ala	Ala	Ala	Asp	Gln	Met	Thr	
			635					640					645			
cgt	ggt	ttc	ctc	ctg	ggc	gcc	acc	gcc	ggt	cgc	acc	acc	ctg	acc	ggt	2442
Arg	Gly	Phe	Leu	Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Leu	Thr	Gly	
		650				655						660				
gag	ggc	ctc	cag	cac	atg	gat	ggc	cac	tcc	ccg	atc	ctg	gcc	tcc	acc	2490
Glu	Gly	Leu	Gln	His	Met	Asp	Gly	His	Ser	Pro	Ile	Leu	Ala	Ser	Thr	
	665					670					675					
aac	ccc	ggt	gtg	gag	acc	tat	gac	ccg	gcg	ttc	tcc	tac	gag	atc	gcg	2538
Asn	Pro	Gly	Val	Glu	Thr	Tyr	Asp	Pro	Ala	Phe	Ser	Tyr	Glu	Ile	Ala	
	680				685					690					695	
cac	ctg	gtc	cac	cgc	ggc	atc	gac	cgc	atg	tac	gga	ccg	ggc	aag	ggt	2586
His	Leu	Val	His	Arg	Gly	Ile	Asp	Arg	Met	Tyr	Gly	Pro	Gly	Lys	Gly	
				700					705					710		
gag	aat	gtc	atc	tac	tac	ctc	acc	atc	tac	aac	gag	cca	acc	ccg	cag	2634
Glu	Asn	Val	Ile	Tyr	Tyr	Leu	Thr	Ile	Tyr	Asn	Glu	Pro	Thr	Pro	Gln	
			715					720					725			
ccg	gct	gag	cct	gag	gat	ctg	gac	gtc	gag	ggc	ctg	cac	aag	ggc	atc	2682
Pro	Ala	Glu	Pro	Glu	Asp	Leu	Asp	Val	Glu	Gly	Leu	His	Lys	Gly	Ile	
		730					735					740				
tac	ctc	tac	gac	aag	gcc	gcc	gag	ggt	gag	ggc	cat	gag	gcc	tcg	atc	2730
Tyr	Leu	Tyr	Asp	Lys	Ala	Ala	Glu	Gly	Glu	Gly	His	Glu	Ala	Ser	Ile	
	745					750					755					

ctg gcc tcc ggc atc ggc atg cag tgg gca ctg cgc gcc cgt gac atc	2778
Leu Ala Ser Gly Ile Gly Met Gln Trp Ala Leu Arg Ala Arg Asp Ile	
760 765 770 775	
ctc gcc gag gat tac ggc atc cgt gcc aac atc ttc tcc gcc acc tcg	2826
Leu Ala Glu Asp Tyr Gly Ile Arg Ala Asn Ile Phe Ser Ala Thr Ser	
780 785 790	
tgg gtg gag ctg gcc cgc gac ggt gcc cgc cgt aac ctg gag gcg ctg	2874
Trp Val Glu Leu Ala Arg Asp Gly Ala Arg Arg Asn Leu Glu Ala Leu	
795 800 805	
cgc aac ccg ggt gcg gat gtc ggt gag gca ttc gtg acc acc cag ctg	2922
Arg Asn Pro Gly Ala Asp Val Gly Glu Ala Phe Val Thr Thr Gln Leu	
810 815 820	
aag aag ggt tcc ggc ccc tac gtc gcg gtg tcc gac ttc gcg acc gac	2970
Lys Lys Gly Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ala Thr Asp	
825 830 835	
ctg ccg aac cag atc cgc gag tgg gtt ccc ggt gac tac atc gtc ctc	3018
Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Ile Val Leu	
840 845 850 855	
ggt gcc gac ggc ttc ggt ttc tcc gat acc cgt ccg gca gcc cgt cgt	3066
Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg	
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Tyr Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Arg Gly	
875 880 885	
ctg gtc cgc gag ggt gtc atc gat gcc tcc gtg gcg gcg cac gcg gct	3162
Leu Val Arg Glu Gly Val Ile Asp Ala Ser Val Ala Ala His Ala Ala	
890 895 900	
gag aag tac aag ctg tcc gac ccg acg gca cca cag gtc gat ccg gac	3210
Glu Lys Tyr Lys Leu Ser Asp Pro Thr Ala Pro Gln Val Asp Pro Asp	
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Ala Pro Ile Glu	
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<210> 22

<211> 923

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 22

Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Thr Asp Asp Thr Asn	
1 5 10 15	
Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp	
20 25 30	
Pro Glu Glu Thr Lys Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln	

		35					40					45				
Asp	Ser	Ser	Pro	Glu	Arg	Ala	Arg	Tyr	Leu	Met	Leu	Arg	Leu	Leu	Glu	
	50					55					60					
Arg	Ala	Ser	Ala	Lys	Arg	Val	Pro	Leu	Pro	Pro	Met	Thr	Ser	Thr	Asp	
65					70					75					80	
Tyr	Val	Asn	Thr	Ile	Pro	Thr	Ser	Met	Glu	Pro	Asp	Phe	Pro	Gly	Asp	
				85					90					95		
Glu	Glu	Met	Glu	Lys	Arg	Tyr	Arg	Arg	Trp	Met	Arg	Trp	Asn	Ala	Ala	
			100					105					110			
Ile	Met	Val	His	Arg	Ala	Gln	Arg	Pro	Gly	Ile	Gly	Val	Gly	Gly	His	
		115					120					125				
Ile	Ser	Thr	Tyr	Ala	Gly	Ala	Ala	Pro	Leu	Tyr	Glu	Val	Gly	Phe	Asn	
	130					135					140					
His	Phe	Phe	Arg	Gly	Lys	Asp	His	Pro	Gly	Gly	Gly	Asp	Gln	Val	Phe	
145					150					155					160	
Phe	Gln	Gly	His	Ala	Ser	Pro	Gly	Met	Tyr	Ala	Arg	Ala	Phe	Leu	Glu	
				165				170						175		
Gly	Arg	Leu	Thr	Glu	Ser	Asp	Leu	Asp	Ser	Phe	Arg	Gln	Glu	Val	Ser	
			180					185					190			
Tyr	Glu	Gly	Gly	Gly	Ile	Pro	Ser	Tyr	Pro	His	Pro	His	Gly	Met	Pro	
		195					200					205				
Asp	Phe	Trp	Glu	Phe	Pro	Thr	Val	Ser	Met	Gly	Leu	Gly	Pro	Met	Asp	
	210					215					220					
Ala	Ile	Tyr	Gln	Ala	Arg	Phe	Asn	Arg	Tyr	Leu	His	Asn	Arg	Gly	Ile	
225					230					235					240	
Lys	Asp	Thr	Ser	Glu	Gln	His	Val	Trp	Ala	Phe	Leu	Gly	Asp	Gly	Glu	
				245				250						255		
Met	Asp	Glu	Pro	Glu	Ser	Arg	Gly	Leu	Ile	His	Gln	Ala	Ala	Leu	Asn	
		260					265						270			
Asn	Leu	Asp	Asn	Leu	Thr	Phe	Val	Ile	Asn	Cys	Asn	Leu	Gln	Arg	Leu	
		275					280					285				
Asp	Gly	Pro	Val	Arg	Gly	Asn	Thr	Lys	Ile	Ile	Gln	Glu	Leu	Glu	Ser	
	290					295					300					
Phe	Phe	Arg	Gly	Ala	Gly	Trp	Ser	Val	Ile	Lys	Val	Ile	Trp	Gly	Arg	
305					310					315					320	
Glu	Trp	Asp	Glu	Leu	Leu	Glu	Lys	Asp	Gln	Asp	Gly	Ala	Leu	Val	Glu	
				325				330						335		
Val	Met	Asn	Asn	Thr	Ser	Asp	Gly	Asp	Tyr	Gln	Thr	Phe	Lys	Ala	Asn	
			340					345					350			
Asp	Gly	Ala	Tyr	Val	Arg	Glu	His	Phe	Phe	Gly	Arg	Asp	Pro	Arg	Thr	
		355					360					365				
Leu	Lys	Leu	Val	Glu	Asp	Met	Thr	Asp	Glu	Glu	Ile	Trp	Lys	Leu	Pro	
	370					375					380					
Arg	Gly	Gly	His	Asp	Tyr	Arg	Lys	Val	Tyr	Ala	Ala	Tyr	Lys	Arg	Ala	
385					390					395					400	
Leu	Glu	Thr	Lys	Asp	Arg	Pro	Thr	Val	Ile	Leu	Ala	His	Thr	Ile	Lys	
				405					410					415		
Gly	Tyr	Gly	Leu	Gly	His	Asn	Phe	Glu	Gly	Arg	Asn	Ala	Thr	His	Gln	
			420					425					430			
Met	Lys	Lys	Leu	Thr	Leu	Asp	Asp	Leu	Lys	Leu	Phe	Arg	Asp	Lys	Gln	
		435					440					445				

Gly	Leu	Pro	Ile	Thr	Asp	Glu	Glu	Leu	Glu	Lys	Asp	Pro	Tyr	Leu	Pro
450						455				460					
Pro	Tyr	Tyr	His	Pro	Gly	Glu	Asp	Ala	Pro	Glu	Ile	Lys	Tyr	Met	Lys
465					470					475					480
Glu	Arg	Arg	Gln	Ala	Leu	Gly	Gly	Phe	Leu	Pro	Glu	Arg	Arg	Glu	Lys
				485					490					495	
Tyr	Glu	Pro	Leu	Gln	Val	Pro	Pro	Leu	Asp	Lys	Leu	Arg	Ser	Val	Arg
			500					505					510		
Lys	Gly	Ser	Gly	Lys	Gln	Gln	Val	Ala	Thr	Thr	Met	Ala	Thr	Val	Arg
		515					520					525			
Thr	Phe	Lys	Glu	Leu	Met	Arg	Asp	Lys	Asn	Leu	Ala	Asp	Arg	Leu	Val
	530					535					540				
Pro	Ile	Ile	Pro	Asp	Glu	Ala	Arg	Thr	Phe	Gly	Leu	Asp	Ser	Trp	Phe
545					550					555					560
Pro	Thr	Leu	Lys	Ile	Tyr	Asn	Pro	His	Gly	Gln	Asn	Tyr	Val	Pro	Val
				565					570					575	
Asp	His	Asp	Leu	Met	Leu	Ser	Tyr	Arg	Glu	Ala	Lys	Asp	Gly	Gln	Ile
			580					585					590		
Leu	His	Glu	Gly	Ile	Asn	Glu	Ala	Gly	Ser	Val	Ala	Ser	Phe	Ile	Ala
		595					600					605			
Ala	Gly	Thr	Ser	Tyr	Ala	Thr	His	Gly	Glu	Ala	Met	Ile	Pro	Leu	Tyr
		610				615					620				
Ile	Phe	Tyr	Ser	Met	Phe	Gly	Phe	Gln	Arg	Thr	Gly	Asp	Gly	Ile	Trp
625					630					635					640
Ala	Ala	Ala	Asp	Gln	Met	Thr	Arg	Gly	Phe	Leu	Leu	Gly	Ala	Thr	Ala
				645					650					655	
Gly	Arg	Thr	Thr	Leu	Thr	Gly	Glu	Gly	Leu	Gln	His	Met	Asp	Gly	His
			660					665					670		
Ser	Pro	Ile	Leu	Ala	Ser	Thr	Asn	Pro	Gly	Val	Glu	Thr	Tyr	Asp	Pro
		675					680					685			
Ala	Phe	Ser	Tyr	Glu	Ile	Ala	His	Leu	Val	His	Arg	Gly	Ile	Asp	Arg
	690					695					700				
Met	Tyr	Gly	Pro	Gly	Lys	Gly	Glu	Asn	Val	Ile	Tyr	Tyr	Leu	Thr	Ile
705					710					715					720
Tyr	Asn	Glu	Pro	Thr	Pro	Gln	Pro	Ala	Glu	Pro	Glu	Asp	Leu	Asp	Val
				725					730					735	
Glu	Gly	Leu	His	Lys	Gly	Ile	Tyr	Leu	Tyr	Asp	Lys	Ala	Ala	Glu	Gly
			740					745					750		
Glu	Gly	His	Glu	Ala	Ser	Ile	Leu	Ala	Ser	Gly	Ile	Gly	Met	Gln	Trp
		755					760					765			
Ala	Leu	Arg	Ala	Arg	Asp	Ile	Leu	Ala	Glu	Asp	Tyr	Gly	Ile	Arg	Ala
		770				775					780				
Asn	Ile	Phe	Ser	Ala	Thr	Ser	Trp	Val	Glu	Leu	Ala	Arg	Asp	Gly	Ala
785					790					795					800
Arg	Arg	Asn	Leu	Glu	Ala	Leu	Arg	Asn	Pro	Gly	Ala	Asp	Val	Gly	Glu
				805					810					815	
Ala	Phe	Val	Thr	Thr	Gln	Leu	Lys	Lys	Gly	Ser	Gly	Pro	Tyr	Val	Ala
			820					825					830		
Val	Ser	Asp	Phe	Ala	Thr	Asp	Leu	Pro	Asn	Gln	Ile	Arg	Glu	Trp	Val
		835					840					845			
Pro	Gly	Asp	Tyr	Ile	Val	Leu	Gly	Ala	Asp	Gly	Phe	Gly	Phe	Ser	Asp

850	855	860
Thr Arg Pro Ala Ala Arg	Arg Tyr Phe Asn Ile	Asp Ala Glu Ser Ile
865	870	875
Val Val Ala Val Leu Arg	Gly Leu Val Arg	Glu Gly Val Ile Asp Ala
885	890	895
Ser Val Ala Ala His Ala	Ala Glu Lys Tyr Lys	Leu Ser Asp Pro Thr
900	905	910
Ala Pro Gln Val Asp Pro	Asp Ala Pro Ile Glu	
915	920	

<210> 23
 <211> 4013
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>
 <221> CDS
 <222> (319)..(3735)

<400> 23

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tctgtaggaa	agtggagccg	ttgggggcaa	cattaacctt	ccccctggga	tgtagctaaa	120
cggcaatggg	ggtctcgggc	ggggggcatt	cttttcacgg	caaggtgggtg	aaattccgca	180
ggtcactccc	cggccggcgg	tagagaacgg	agcgaaaacg	gaaagcaata	cgtgggttttc	240
cggactggcc	gttacgatgt	tctgaagagt	gactgccatc	acccaacagg	ctggtcctcg	300
tcgaaaggaa	caaaaact	gtg gtt aca	aca aca ccc	tcc acg ctg	ccg gcg	351
	Val Val Thr	Thr Thr Thr	Pro Ser Thr	Leu Pro Ala		
	1	5	10			
ttc aaa aag	atc ctg gtg	gcc aac cga	ggt gaa atc	gcg gtg cga	gca	399
Phe Lys Lys	Ile Leu Val	Ala Asn Arg	Gly Glu Ile	Ala Val Arg	Ala	
	15	20	25			
ttc cgc gcc	gcc tac gag	acc ggg gcc	gca acc gtg	gcc atc tac	ccc	447
Phe Arg Ala	Ala Tyr Glu	Thr Gly Ala	Ala Thr Val	Ala Ile Tyr	Pro	
	30	35	40			
cgg gag gac	cgt ggc tcc	ttc cac cgc	tcc ttc gcc	tcc gag gcg	gtg	495
Arg Glu Asp	Arg Gly Ser	Phe His Arg	Ser Phe Ala	Ser Glu Ala	Val	
	45	50	55			
agg atc gga	acc gag ggc	tca ccc gtc	aag gcg tac	ctc gat att	gat	543
Arg Ile Gly	Thr Glu Gly	Ser Pro Val	Lys Ala Tyr	Leu Asp Ile	Asp	
	60	65	70			
gag atc atc	aac gcc gcc	aag aag gtg	aaa gcg gac	gcg gtc tac	ccg	591
Glu Ile Ile	Asn Ala Ala	Lys Lys Val	Lys Ala Asp	Ala Val Tyr	Pro	
	80	85	90			
ggg tat ggt	ttc ctt tcg	gaa aat gcc	cag ctc gcg	cgt gaa tgc	gcg	639
Gly Tyr Gly	Phe Leu Ser	Glu Asn Ala	Gln Leu Ala	Arg Glu Cys	Ala	
	95	100	105			
gag aac ggc	att acc ttc	atc ggt ccc	acc ccg gag	gtg ctc gac	ctc	687
Glu Asn Gly	Ile Thr Phe	Ile Gly Pro	Thr Pro Glu	Val Leu Asp	Leu	
	110	115	120			
acg ggc gac	aag tcc aag	gct gtg tcc	gcc gcg aag	aag gcc ggg	ctg	735
Thr Gly Asp	Lys Ser Lys	Ala Val Ser	Ala Ala Lys	Lys Ala Gly	Leu	

125	130	135	
ccg gtg ctg gcg gaa tcc acc ccc agc acc gac atc gat gag atc gtc			783
Pro Val Leu Ala Glu Ser Thr Pro Ser Thr Asp Ile Asp Glu Ile Val			
140	145	150	155
aag agt gcc gag ggg cag acc tac ccg atc ttc gtc aag gcc gtc gca			831
Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala			
160	165	170	
ggt ggt ggc ggg cgt ggt atg cgg ttc gtc gag aag ccc gag gac ctg			879
Gly Gly Gly Gly Arg Gly Met Arg Phe Val Glu Lys Pro Glu Asp Leu			
175	180	185	
cgt gag ctg gcc agg gag gcc tcc cgc gag gcg gag gcc gct ttc ggt			927
Arg Glu Leu Ala Arg Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly			
190	195	200	
gac gga tcc gtc tac gtc gaa cgg gcc gtg atc aaa ccc cag cac atc			975
Asp Gly Ser Val Tyr Val Glu Arg Ala Val Ile Lys Pro Gln His Ile			
205	210	215	
gag gtg cag atc ctc ggt gat cac acc ggc gat gtc atc cac ctg tat			1023
Glu Val Gln Ile Leu Gly Asp His Thr Gly Asp Val Ile His Leu Tyr			
220	225	230	235
gaa cgc gac tgt tcc ctg cag cgc cgc cac cag aag gtc gtg gag atc			1071
Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile			
240	245	250	
gca cct gcc cag cac ctc gac ccg gag ctg cgc gac cgc atc tgt gcc			1119
Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala			
255	260	265	
gat gcc gtg aag ttc tgc aaa tcc atc gga tac cag ggc gcc ggc acc			1167
Asp Ala Val Lys Phe Cys Lys Ser Ile Gly Tyr Gln Gly Ala Gly Thr			
270	275	280	
gtg gag ttc ctc gtc gac gag gcg ggc aac cac gtc ttc att gag atg			1215
Val Glu Phe Leu Val Asp Glu Ala Gly Asn His Val Phe Ile Glu Met			
285	290	295	
aac ccc cgc atc cag gtg gaa cac acc gtg acc gag gag gtc acc tcc			1263
Asn Pro Arg Ile Gln Val Glu His Thr Val Thr Glu Glu Val Thr Ser			
300	305	310	315
gtc gac ctg gtc aag gcg cag atg cac ctg gcc gcc ggt gcc acc ctg			1311
Val Asp Leu Val Lys Ala Gln Met His Leu Ala Ala Gly Ala Thr Leu			
320	325	330	
aag gaa ctg ggc ctg acc cag gac aag atc acc acc cac ggt gcc gcc			1359
Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Thr Thr His Gly Ala Ala			
335	340	345	
ctg cag tgc cgc atc acc acg gag gac ccg tcc aac aac ttc cgg ccc			1407
Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Ser Asn Asn Phe Arg Pro			
350	355	360	
gac acc ggt gtg atc acc gcc tac cgc tcc ccg ggt ggt gcg ggt gtg			1455
Asp Thr Gly Val Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val			
365	370	375	
cgt ctc gac ggc gca gcc cag ctc ggc ggc gag atc acc gca cat ttc			1503
Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe			
380	385	390	395
gat tcc atg ctg gtc aag atg acc tgc cgc ggt tcc gat ttc gag acc			1551
Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr			

				400				405					410				
gcc	gtg	tcc	cga	gcc	cag	cgc	gcc	ctg	gcg	gag	ttc	aac	gtc	tcc	ggc		1599
Ala	Val	Ser	Arg	Ala	Gln	Arg	Ala	Leu	Ala	Glu	Phe	Asn	Val	Ser	Gly		
			415					420					425				
gtg	gcc	acc	aac	atc	ggc	ttc	ctg	cgt	gcg	ctg	ctg	cgc	gag	gaa	gac		1647
Val	Ala	Thr	Asn	Ile	Gly	Phe	Leu	Arg	Ala	Leu	Leu	Arg	Glu	Glu	Asp		
			430					435					440				
ttc	acc	aag	agg	cgc	atc	gac	acc	ggc	ttc	atc	ggc	tcc	cac	cag	cac		1695
Phe	Thr	Lys	Arg	Arg	Ile	Asp	Thr	Gly	Phe	Ile	Gly	Ser	His	Gln	His		
			445					450					455				
ctg	ctc	cag	gcc	cca	ccg	gcc	gac	gat	gag	cag	ggg	cgg	atc	ctg	gaa		1743
Leu	Leu	Gln	Ala	Pro	Pro	Ala	Asp	Asp	Glu	Gln	Gly	Arg	Ile	Leu	Glu		
460																475	
tac	ctg	gcg	gat	gtc	acc	gtg	aac	aaa	ccc	cac	ggg	gaa	cgc	ccc	gag		1791
Tyr	Leu	Ala	Asp	Val	Thr	Val	Asn	Lys	Pro	His	Gly	Glu	Arg	Pro	Glu		
				480												490	
aca	gcc	cgt	ccg	ata	gag	aag	ctg	ccc	gag	gtg	gag	aac	atc	ccg	ctg		1839
Thr	Ala	Arg	Pro	Ile	Glu	Lys	Leu	Pro	Glu	Val	Glu	Asn	Ile	Pro	Leu		
				495												505	
cca	cgc	ggc	tcc	cgc	gac	cgc	ctg	aag	cag	ctc	ggc	ccg	gag	ggg	ttc		1887
Pro	Arg	Gly	Ser	Arg	Asp	Arg	Leu	Lys	Gln	Leu	Gly	Pro	Glu	Gly	Phe		
				510												520	
gcc	cgc	gat	ctg	cgc	gaa	cag	gat	gcc	ctg	gcc	gtc	acc	gac	acc	acc		1935
Ala	Arg	Asp	Leu	Arg	Glu	Gln	Asp	Ala	Leu	Ala	Val	Thr	Asp	Thr	Thr		
				525												535	
ttc	cgc	gat	gcc	cac	cag	tcc	ctc	ctg	gcc	acc	cgc	gtg	cgc	tcc	ttc		1983
Phe	Arg	Asp	Ala	His	Gln	Ser	Leu	Leu	Ala	Thr	Arg	Val	Arg	Ser	Phe		
				540												555	
gcg	ctg	acc	ccg	gcg	gcg	cgc	gcc	gtc	gca	aag	ctc	acc	ccc	gag	ctg		2031
Ala	Leu	Thr	Pro	Ala	Ala	Arg	Ala	Val	Ala	Lys	Leu	Thr	Pro	Glu	Leu		
				560												570	
ctg	tcg	gtg	gag	gcc	tgg	ggc	ggg	gcc	acc	tac	gac	gtg	gcc	atg	cgc		2079
Leu	Ser	Val	Glu	Ala	Trp	Gly	Gly	Ala	Thr	Tyr	Asp	Val	Ala	Met	Arg		
				575												585	
ttc	ctc	ttc	gag	gat	ccg	tgg	gca	cgc	ctg	gat	gag	ctg	cgt	gag	gcg		2127
Phe	Leu	Phe	Glu	Asp	Pro	Trp	Ala	Arg	Leu	Asp	Glu	Leu	Arg	Glu	Ala		
				590												600	
atg	ccg	aat	gtg	aac	atc	cag	atg	ctg	ctg	cgt	ggg	cgc	aac	acc	gtc		2175
Met	Pro	Asn	Val	Asn	Ile	Gln	Met	Leu	Leu	Arg	Gly	Arg	Asn	Thr	Val		
				605												615	
ggg	tac	acc	ccg	tac	ccc	gat	tcg	gtg	tgc	cgc	gcg	ttt	gtg	cag	gag		2223
Gly	Tyr	Thr	Pro	Tyr	Pro	Asp	Ser	Val	Cys	Arg	Ala	Phe	Val	Gln	Glu		
				620												635	
gcc	gcc	aag	tcc	ggg	gtg	gac	atc	ttc	cgc	atc	ttc	gac	gcg	ctc	aac		2271
Ala	Ala	Lys	Ser	Gly	Val	Asp	Ile	Phe	Arg	Ile	Phe	Asp	Ala	Leu	Asn		
				640												650	
gac	atc	tcc	cag	atg	cgc	ccg	gcc	atc	gac	gcc	gtc	ctg	gag	acc	ggc		2319
Asp	Ile	Ser	Gln	Met	Arg	Pro	Ala	Ile	Asp	Ala	Val	Leu	Glu	Thr	Gly		
				655												665	
acc	agt	gtt	gcc	gag	gtc	gcc	atg	gcg	tac	tcc	ggg	gac	ctg	tcc	aat		2367
Thr	Ser	Val	Ala	Glu	Val	Ala	Met	Ala	Tyr	Ser	Gly	Asp	Leu	Ser	Asn		

670	675	680	
ccg ggg gag aag ctc tac acc ctg gac tac tac ctg aac ctg gcc gag			2415
Pro Gly Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu Asn Leu Ala Glu			
685	690	695	
cag atc gtc gac tcc ggt gca cac atc ctg gcc atc aag gac atg gcc			2463
Gln Ile Val Asp Ser Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala			
700	705	710	715
ggc ctg ctg cgc cgc gcc gcg gcg ccc aaa ctg gtc acc gcc ctg cgc			2511
Gly Leu Leu Arg Arg Ala Ala Ala Pro Lys Leu Val Thr Ala Leu Arg			
	720	725	730
cgt gaa ttc gac ctg ccc gtg cat gtc cac acc cac gac acc gcc ggc			2559
Arg Glu Phe Asp Leu Pro Val His Val His Thr His Asp Thr Ala Gly			
	735	740	745
ggt cag ctg gcc acc tac ctg gcc gcc gcc aac gcc ggg gcc gat gcc			2607
Gly Gln Leu Ala Thr Tyr Leu Ala Ala Ala Asn Ala Gly Ala Asp Ala			
	750	755	760
gtc gac gcc gcc tcc gca ccc ctg tcc ggt acc acc tcc cag ccg tcg			2655
Val Asp Ala Ala Ser Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser			
	765	770	775
atg tcc gct ctg gtt gcc gcg ttt gcg cac acc cga cgc gac acc ggc			2703
Met Ser Ala Leu Val Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly			
	780	785	790
ctc aac ctg cag gcc gtc tcc gac ctg gaa ccg tac tgg gag gcg gtc			2751
Leu Asn Leu Gln Ala Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val			
	800	805	810
cgc gga ctg tac ctg ccg ttt gaa tcc ggc acc ccg ggc ccg acc gga			2799
Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly			
	815	820	825
cgc gtt tac cgc cac gag atc ccc ggc ggt cag ctg tcc aac ctg cgt			2847
Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg			
	830	835	840
gcc cag gcc gtt gca ctg ggt ctg gcc gac cgc ttc gag ctc atc gag			2895
Ala Gln Ala Val Ala Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu			
	845	850	855
gac tac tac gcg gcc gtc aac gag atg ctg ggt cgt ccg acc aag gtc			2943
Asp Tyr Tyr Ala Ala Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val			
	860	865	870
acc ccg tcc tcc aag gtt gtc ggt gac ctc gca ctg cac ctc gtc ggt			2991
Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His Leu Val Gly			
	880	885	890
gcc ggt gtg agc ccg gag gat ttc gcc gcc gat ccg cag aag tac gac			3039
Ala Gly Val Ser Pro Glu Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp			
	895	900	905
atc ccc gat tcg gtc atc gcc ttc ctc cgc ggc gaa ctg ggt acc cct			3087
Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu Gly Thr Pro			
	910	915	920
ccc ggt ggc tgg ccc gaa ccg ctg cgc acc cgt gca ctc gag ggt cgc			3135
Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg			
	925	930	935
tcc cag ggt aag gcc ccg ctg gcg gag atc ccc gcc gag gag cag gcc			3183
Ser Gln Gly Lys Ala Pro Leu Ala Glu Ile Pro Ala Glu Glu Gln Ala			

940		945		950		955	
cac ctg gat tcc gat	gat tcc gcg gag cgt	cgc ggc acc ctc aac cgc	3231				
His Leu Asp Ser Asp	Asp Ser Ala Glu Arg Arg	Gly Thr Leu Asn Arg					
	960	965	970				
ctg ctg ttc ccg aag ccg acc gag gag	ttc ctt gag cac cgt cgc cgc	3279					
Leu Leu Phe Pro Lys Pro Thr Glu Glu	Phe Leu Glu His Arg Arg Arg						
	975	980	985				
ttc ggc aac acc tcc gcc ctg gat gac	cgc gag ttc ttc tac ggc ttg	3327					
Phe Gly Asn Thr Ser Ala Leu Asp Asp	Arg Glu Phe Phe Tyr Gly Leu						
	990	995	1000				
aag gag gga cgt gag gag ctg atc cga	ctg acc ggt gtg tcc acc ccg	3375					
Lys Glu Gly Arg Glu Glu Leu Ile Arg	Leu Thr Gly Val Ser Thr Pro						
	1005	1010	1015				
atg gtg gtc cgc ctg gat gcg gtg tcc	gaa ccg gat gac aaa ggc atg	3423					
Met Val Val Arg Leu Asp Ala Val Ser	Glu Pro Asp Asp Lys Gly Met						
	1020	1025	1030				
cgc aac gtg gtg gtc aac gtc aac ggc	cag atc cgc ccg atc aag gtg	3471					
Arg Asn Val Val Val Asn Val Asn Gly	Gln Ile Arg Pro Ile Lys Val						
	1040	1045	1050				
cgc gac cgt tcc gtg gag tcc gtc acc	gcc acc gcg gag aag gcc gat	3519					
Arg Asp Arg Ser Val Glu Ser Val Thr	Ala Thr Ala Glu Lys Ala Asp						
	1055	1060	1065				
gcc acc aac aag ggc cat gtc gcc gca	cca ttc gcc ggt gtg gtc acc	3567					
Ala Thr Asn Lys Gly His Val Ala Ala	Pro Phe Ala Gly Val Val Thr						
	1070	1075	1080				
gtg acc gtc gcc gag ggt gat gag atc	aag gct ggc gac gcc gtg gcc	3615					
Val Thr Val Ala Glu Gly Asp Glu Ile	Lys Ala Gly Asp Ala Val Ala						
	1085	1090	1095				
atc att gag gcc atg aag atg gag gcc	acc atc acc gcg cct gtc gac	3663					
Ile Ile Glu Ala Met Lys Met Glu Ala	Thr Ile Thr Ala Pro Val Asp						
	1100	1105	1110				
ggt gtc atc gac cgc gtc gtg gtg ccc	gcc gcc acc aag gtc gag ggc	3711					
Gly Val Ile Asp Arg Val Val Val Pro	Ala Ala Thr Lys Val Glu Gly						
	1120	1125	1130				
ggc gac ctc atc gtg gtc gtg tcc	tagcgactga gagccacaac ccgtcccggg	3765					
Gly Asp Leu Ile Val Val Val Ser							
	1135						
tgccttgтта tcaacctccc cctgatgatg	ttctcagggg gaggctctac gtacctcacc	3825					
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cccactccgt gatgtcccgt gctgatccca	ggcaggccgg ttggaaagaa aaaccagtga	3945					
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<210> 24

<211> 1139

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 24

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		20						25					30		
Glu	Thr	Gly	Ala	Ala	Thr	Val	Ala	Ile	Tyr	Pro	Arg	Glu	Asp	Arg	Gly
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Ser	Phe	His	Arg	Ser	Phe	Ala	Ser	Glu	Ala	Val	Arg	Ile	Gly	Thr	Glu
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Gly	Ser	Pro	Val	Lys	Ala	Tyr	Leu	Asp	Ile	Asp	Glu	Ile	Ile	Asn	Ala
65					70					75					80
Ala	Lys	Lys	Val	Lys	Ala	Asp	Ala	Val	Tyr	Pro	Gly	Tyr	Gly	Phe	Leu
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Ser	Glu	Asn	Ala	Gln	Leu	Ala	Arg	Glu	Cys	Ala	Glu	Asn	Gly	Ile	Thr
			100					105					110		
Phe	Ile	Gly	Pro	Thr	Pro	Glu	Val	Leu	Asp	Leu	Thr	Gly	Asp	Lys	Ser
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Lys	Ala	Val	Ser	Ala	Ala	Lys	Lys	Ala	Gly	Leu	Pro	Val	Leu	Ala	Glu
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Ser	Thr	Pro	Ser	Thr	Asp	Ile	Asp	Glu	Ile	Val	Lys	Ser	Ala	Glu	Gly
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Gln	Thr	Tyr	Pro	Ile	Phe	Val	Lys	Ala	Val	Ala	Gly	Gly	Gly	Gly	Arg
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Gly	Met	Arg	Phe	Val	Glu	Lys	Pro	Glu	Asp	Leu	Arg	Glu	Leu	Ala	Arg
			180					185					190		
Glu	Ala	Ser	Arg	Glu	Ala	Glu	Ala	Ala	Phe	Gly	Asp	Gly	Ser	Val	Tyr
		195					200					205			
Val	Glu	Arg	Ala	Val	Ile	Lys	Pro	Gln	His	Ile	Glu	Val	Gln	Ile	Leu
	210					215					220				
Gly	Asp	His	Thr	Gly	Asp	Val	Ile	His	Leu	Tyr	Glu	Arg	Asp	Cys	Ser
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Leu	Gln	Arg	Arg	His	Gln	Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln	His
				245					250					255	
Leu	Asp	Pro	Glu	Leu	Arg	Asp	Arg	Ile	Cys	Ala	Asp	Ala	Val	Lys	Phe
			260					265					270		
Cys	Lys	Ser	Ile	Gly	Tyr	Gln	Gly	Ala	Gly	Thr	Val	Glu	Phe	Leu	Val
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Asp	Glu	Ala	Gly	Asn	His	Val	Phe	Ile	Glu	Met	Asn	Pro	Arg	Ile	Gln
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Val	Glu	His	Thr	Val	Thr	Glu	Glu	Val	Thr	Ser	Val	Asp	Leu	Val	Lys
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Ala	Gln	Met	His	Leu	Ala	Ala	Gly	Ala	Thr	Leu	Lys	Glu	Leu	Gly	Leu
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Thr	Gln	Asp	Lys	Ile	Thr	Thr	His	Gly	Ala	Ala	Leu	Gln	Cys	Arg	Ile
			340					345					350		
Thr	Thr	Glu	Asp	Pro	Ser	Asn	Asn	Phe	Arg	Pro	Asp	Thr	Gly	Val	Ile
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Thr	Ala	Tyr	Arg	Ser	Pro	Gly	Gly	Ala	Gly	Val	Arg	Leu	Asp	Gly	Ala
	370					375					380				
Ala	Gln	Leu	Gly	Gly	Glu	Ile	Thr	Ala	His	Phe	Asp	Ser	Met	Leu	Val
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Lys	Met	Thr	Cys	Arg	Gly	Ser	Asp	Phe	Glu	Thr	Ala	Val	Ser	Arg	Ala
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Gln	Arg	Ala	Leu	Ala	Glu	Phe	Asn	Val	Ser	Gly	Val	Ala	Thr	Asn	Ile

			420					425					430						
Gly	Phe	Leu	Arg	Ala	Leu	Leu	Arg	Glu	Glu	Asp	Phe	Thr	Lys	Arg	Arg				
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Ile	Asp	Thr	Gly	Phe	Ile	Gly	Ser	His	Gln	His	Leu	Leu	Gln	Ala	Pro				
	450					455					460								
Pro	Ala	Asp	Asp	Glu	Gln	Gly	Arg	Ile	Leu	Glu	Tyr	Leu	Ala	Asp	Val				
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Thr	Val	Asn	Lys	Pro	His	Gly	Glu	Arg	Pro	Glu	Thr	Ala	Arg	Pro	Ile				
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Glu	Lys	Leu	Pro	Glu	Val	Glu	Asn	Ile	Pro	Leu	Pro	Arg	Gly	Ser	Arg				
		500					505						510						
Asp	Arg	Leu	Lys	Gln	Leu	Gly	Pro	Glu	Gly	Phe	Ala	Arg	Asp	Leu	Arg				
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Glu	Gln	Asp	Ala	Leu	Ala	Val	Thr	Asp	Thr	Thr	Phe	Arg	Asp	Ala	His				
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Gln	Ser	Leu	Leu	Ala	Thr	Arg	Val	Arg	Ser	Phe	Ala	Leu	Thr	Pro	Ala				
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Ala	Arg	Ala	Val	Ala	Lys	Leu	Thr	Pro	Glu	Leu	Leu	Ser	Val	Glu	Ala				
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Trp	Gly	Gly	Ala	Thr	Tyr	Asp	Val	Ala	Met	Arg	Phe	Leu	Phe	Glu	Asp				
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Pro	Trp	Ala	Arg	Leu	Asp	Glu	Leu	Arg	Glu	Ala	Met	Pro	Asn	Val	Asn				
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Ile	Gln	Met	Leu	Leu	Arg	Gly	Arg	Asn	Thr	Val	Gly	Tyr	Thr	Pro	Tyr				
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Pro	Asp	Ser	Val	Cys	Arg	Ala	Phe	Val	Gln	Glu	Ala	Ala	Lys	Ser	Gly				
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Arg	Pro	Ala	Ile	Asp	Ala	Val	Leu	Glu	Thr	Gly	Thr	Ser	Val	Ala	Glu				
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Val	Ala	Met	Ala	Tyr	Ser	Gly	Asp	Leu	Ser	Asn	Pro	Gly	Glu	Lys	Leu				
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Tyr	Thr	Leu	Asp	Tyr	Tyr	Leu	Asn	Leu	Ala	Glu	Gln	Ile	Val	Asp	Ser				
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Pro	Val	His	Val	His	Thr	His	Asp	Thr	Ala	Gly	Gly	Gln	Leu	Ala	Thr				
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Tyr	Leu	Ala	Ala	Ala	Asn	Ala	Gly	Ala	Asp	Ala	Val	Asp	Ala	Ala	Ser				
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Ala	Pro	Leu	Ser	Gly	Thr	Thr	Ser	Gln	Pro	Ser	Met	Ser	Ala	Leu	Val				
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Val	Ser	Asp	Leu	Glu	Pro	Tyr	Trp	Glu	Ala	Val	Arg	Gly	Leu	Tyr	Leu				
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Pro	Phe	Glu	Ser	Gly	Thr	Pro	Gly	Pro	Thr	Gly	Arg	Val	Tyr	Arg	His				
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Glu	Ile	Pro	Gly	Gly	Gln	Leu	Ser	Asn	Leu	Arg	Ala	Gln	Ala	Val	Ala		
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Leu	Gly	Leu	Ala	Asp	Arg	Phe	Glu	Leu	Ile	Glu	Asp	Tyr	Tyr	Ala	Ala		
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Val	Val	Gly	Asp	Leu	Ala	Leu	His	Leu	Val	Gly	Ala	Gly	Val	Ser	Pro		
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Glu	Asp	Phe	Ala	Ala	Asp	Pro	Gln	Lys	Tyr	Asp	Ile	Pro	Asp	Ser	Val		
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Ile	Ala	Phe	Leu	Arg	Gly	Glu	Leu	Gly	Thr	Pro	Pro	Gly	Gly	Trp	Pro		
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Pro	Thr	Glu	Glu	Phe	Leu	Glu	His	Arg	Arg	Arg	Phe	Gly	Asn	Thr	Ser		
		980						985					990				
Ala	Leu	Asp	Asp	Arg	Glu	Phe	Phe	Tyr	Gly	Leu	Lys	Glu	Gly	Arg	Glu		
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Asp	Ala	Val	Ser	Glu	Pro	Asp	Asp	Lys	Gly	Met	Arg	Asn	Val	Val	Val		
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Asn	Val	Asn	Gly	Gln	Ile	Arg	Pro	Ile	Lys	Val	Arg	Asp	Arg	Ser	Val		
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Glu	Ser	Val	Thr	Ala	Thr	Ala	Glu	Lys	Ala	Asp	Ala	Thr	Asn	Lys	Gly		
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His	Val	Ala	Ala	Pro	Phe	Ala	Gly	Val	Val	Thr	Val	Thr	Val	Ala	Glu		
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Gly	Asp	Glu	Ile	Lys	Ala	Gly	Asp	Ala	Val	Ala	Ile	Ile	Glu	Ala	Met		
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Lys	Met	Glu	Ala	Thr	Ile	Thr	Ala	Pro	Val	Asp	Gly	Val	Ile	Asp	Arg		
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Val Asn Glu Leu Leu Arg Asp Asp Ile Arg Tyr Leu Gly Arg Ile	
1 5 10 15	
ctg ggc gag gtg atc tcc gag cag gag ggc cac cat gtc ttc gaa ctg	156
Leu Gly Glu Val Ile Ser Glu Gln Glu Gly His His Val Phe Glu Leu	
20 25 30	
gtt gaa cgc gcc cgc cgg acc tcc ttc gac atc gcc aag gga cgc gcg	204
Val Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala	
35 40 45	
gag atg gac agt ctg gtg gag gtg ttc gct ggc atc gac ccg gag gac	252
Glu Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp	
50 55 60	
gcc acg ccc gtg gcc cga gcc ttc acc cat ttc gcc ctg ttg gcc aac	300
Ala Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn	
65 70 75	
ctc gcg gag gat ttg cat gac gca gcc cag cgg gaa cag gcc ctg aac	348
Leu Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn	
80 85 90 95	
tcg ggt gag ccc gcg ccg gac agc acc ctc gag gcc acc tgg gtg aaa	396
Ser Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys	
100 105 110	
ctg gat gat gcc ggg gtg ggc agc ggt gag gtc gcc gcg gtg atc cgc	444
Leu Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg	
115 120 125	
aat gcg ctc gtc gcc ccg gtg ctc acc gcg cac ccg acg gaa acc cga	492
Asn Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg	
130 135 140	
cgt cgt acc gtg ttc gac gcg cag aag cac atc acc gcc ctg atg gag	540
Arg Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu	
145 150 155	
gaa cgc cac ctc ctc ctg gcg ctg ccc acg cat gcc cgg acc cag tcc	588
Glu Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser	
160 165 170 175	
aag ctg gat gac atc gag cgc aac atc cgg cga cgg atc acg atc ctg	636
Lys Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu	
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tgg cag acg gcc ctc atc cgt gtg gcc cgt ccc cgc atc gag gat gag	684
Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu	
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Val Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile	
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Pro Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly	
225 230 235	
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Gly Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly	
240 245 250 255	
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Gly Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr	

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Ala	Thr	His	Arg	Ala	Ala	Glu	Thr	Val	Leu	Lys	Tyr	Tyr	Val	Lys	Gln		
			275					280					285				
ctg	cac	gcc	ctg	gaa	cac	gaa	ctc	agt	ctc	tcc	gac	cgg	atg	aac	gtc		972
Leu	His	Ala	Leu	Glu	His	Glu	Leu	Ser	Leu	Ser	Asp	Arg	Met	Asn	Val		
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atc	agc	gat	gag	ctg	cgt	gtg	ctt	gcc	gat	gcc	ggc	cag	aat	gac	atg		1020
Ile	Ser	Asp	Glu	Leu	Arg	Val	Leu	Ala	Asp	Ala	Gly	Gln	Asn	Asp	Met		
	305					310					315						
ccc	agc	cgg	gtt	gat	gaa	ccc	tac	cgg	cgg	gcc	atc	cac	ggc	atg	cgt		1068
Pro	Ser	Arg	Val	Asp	Glu	Pro	Tyr	Arg	Arg	Ala	Ile	His	Gly	Met	Arg		
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ggc	cgg	atg	ctg	gcc	acc	acg	gcc	gcc	ctg	atc	ggg	gag	gag	gcg	gtc		1116
Gly	Arg	Met	Leu	Ala	Thr	Thr	Ala	Ala	Leu	Ile	Gly	Glu	Glu	Ala	Val		
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gag	ggc	acc	tgg	ttc	aag	acc	ttc	acg	ccc	tat	acc	gat	acc	cac	gag		1164
Glu	Gly	Thr	Trp	Phe	Lys	Thr	Phe	Thr	Pro	Tyr	Thr	Asp	Thr	His	Glu		
			355				360						365				
ttc	aaa	cgc	gac	ctc	gat	atc	gtg	gat	ggg	tcc	ctg	aga	atg	tcc	cgg		1212
Phe	Lys	Arg	Asp	Leu	Asp	Ile	Val	Asp	Gly	Ser	Leu	Arg	Met	Ser	Arg		
			370				375					380					
gat	gac	atc	atc	gcc	gat	gac	cgt	ctg	gcc	atg	ctg	cgc	tcg	gcc	ctg		1260
Asp	Asp	Ile	Ile	Ala	Asp	Asp	Arg	Leu	Ala	Met	Leu	Arg	Ser	Ala	Leu		
	385					390					395						
gac	agc	ttc	ggg	ttc	aac	ctc	tac	tcc	ctg	gat	ctg	cgc	cag	aat	tcc		1308
Asp	Ser	Phe	Gly	Phe	Asn	Leu	Tyr	Ser	Leu	Asp	Leu	Arg	Gln	Asn	Ser		
	400				405					410					415		
gac	ggg	ttc	gag	gat	gtc	ctc	acc	gaa	ttg	ttc	gcc	acc	gcc	cag	acc		1356
Asp	Gly	Phe	Glu	Asp	Val	Leu	Thr	Glu	Leu	Phe	Ala	Thr	Ala	Gln	Thr		
			420					425						430			
gag	aag	aac	tac	cgc	ggg	ttg	acg	gag	gcg	gag	aag	ctg	gac	ctg	ctg		1404
Glu	Lys	Asn	Tyr	Arg	Gly	Leu	Thr	Glu	Ala	Glu	Lys	Leu	Asp	Leu	Leu		
			435				440						445				
atc	cgc	gaa	ctg	agc	aca	ccc	cgc	ccg	ctc	atc	ccg	cac	ggg	gac	ccg		1452
Ile	Arg	Glu	Leu	Ser	Thr	Pro	Arg	Pro	Leu	Ile	Pro	His	Gly	Asp	Pro		
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gac	tac	tcc	gag	gcc	acc	aac	cgt	gaa	ctg	ggg	att	ttt	tcg	aag	gcc		1500
Asp	Tyr	Ser	Glu	Ala	Thr	Asn	Arg	Glu	Leu	Gly	Ile	Phe	Ser	Lys	Ala		
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Ala	Glu	Ala	Val	Arg	Lys	Phe	Gly	Pro	Leu	Met	Val	Pro	His	Cys	Ile		
	480				485					490					495		
atc	tcc	atg	gcc	tct	tcc	gtc	acg	gac	atc	ctc	gaa	ccg	atg	gtg	ctg		1596
Ile	Ser	Met	Ala	Ser	Ser	Val	Thr	Asp	Ile	Leu	Glu	Pro	Met	Val	Leu		
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ctc	aag	gag	ttc	ggg	ctg	atc	cgg	gcc	aac	ggg	aag	aac	ccg	acg	ggc		1644
Leu	Lys	Glu	Phe	Gly	Leu	Ile	Arg	Ala	Asn	Gly	Lys	Asn	Pro	Thr	Gly		
			515				520						525				
agc	gtc	gac	gtg	atc	ccg	ctg	ttc	gag	acg	atc	gat	gac	ctc	cag	cgt		1692
Ser	Val	Asp	Val	Ile	Pro	Leu	Phe	Glu	Thr	Ile	Asp	Asp	Leu	Gln	Arg		

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Gly Ala Gly Ile Leu Glu Glu Leu Trp Asp Ile Asp Leu Tyr Arg Asn			
545	550	555	
tac ctt gag cag cgg gac aac gtc cag gag gtc atg ctg ggg tat tcc			1788
Tyr Leu Glu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser			
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gac tcc aac aag gac ggc ggg tac ttc gcc gcc aac tgg gcg ctt tac			1836
Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp Ala Leu Tyr			
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gac gcg gag tta cgc ctg gtc gaa cta tgc cgg ggc cgt aat gtc aag			1884
Asp Ala Glu Leu Arg Leu Val Glu Leu Cys Arg Gly Arg Asn Val Lys			
595	600	605	
ctc cgt ctc ttc cac ggt cgt ggt ggc acg gtg ggt cgt ggc ggt ggc			1932
Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly			
610	615	620	
ccc tcc tat gat gcg atc ctg gcc cag ccc aag ggc gcg gtc cgg ggt			1980
Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Lys Gly Ala Val Arg Gly			
625	630	635	
gcg gtg cgg gtg act gaa cag ggc gag atc atc tcc gcg aag tac ggt			2028
Ala Val Arg Val Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly			
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aac ccg gat acg gca cgc cgc aac ctt gag gcc ctg gtg tcc gcg acg			2076
Asn Pro Asp Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr			
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ctg gag gca tcg ctt ctg gat gat gtg gaa ctg ccc aat cgg gaa cgc			2124
Leu Glu Ala Ser Leu Leu Asp Asp Val Glu Leu Pro Asn Arg Glu Arg			
675	680	685	
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Ala His Gln Ile Met Gly Glu Ile Ser Glu Leu Ser Phe Arg Arg Tyr			
690	695	700	
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Ser Ser Leu Val His Glu Asp Pro Gly Phe Ile Gln Tyr Phe Thr Gln			
705	710	715	
tcc acc ccc ctg cag gag atc gga tcc ctc aac atc ggt tcc cga ccc			2268
Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro			
720	725	730	735
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Ser Ser Arg Lys Gln Thr Asn Thr Val Glu Asp Leu Arg Ala Ile Pro			
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Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe			
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Gly Val Gly Thr Ala Leu Arg Glu Trp Ile Gly Glu Gly Glu Gly Ala			
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Ala Glu Arg Ile Ala Glu Leu Gln Glu Leu Asn Arg Cys Trp Pro Phe			
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Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu			

Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg Asn
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 Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg Arg
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 Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu Glu
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 Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser Lys
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 Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu Trp
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 Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu Val
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 Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile Pro
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 Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly Gly
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 Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly Gly
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 Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr Ala
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 Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln Leu
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 Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr Glu
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 465 470 475 480
 Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile Ile
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 <213> Corynebacterium thermoaminogenes

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 Met Ala Ser Asn Phe Lys Glu Thr Ala
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 Lys Lys Gln Phe Asp Leu Asn Gly Gln Ser Tyr Thr Tyr Tyr Asp Leu
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 aaa tca tta gaa gaa caa ggt tta act aaa att tca aag tta cct tat 808
 Lys Ser Leu Glu Glu Gln Gly Leu Thr Lys Ile Ser Lys Leu Pro Tyr
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 Ser Ile Arg Val Leu Leu Glu Ser Val Leu Arg Gln Glu Asp Asp Phe
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 Val Ile Thr Asp Asp His Ile Lys Gln Leu Ala Glu Phe Gly Lys Lys
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 Gly Asn Glu Gly Glu Val Pro Phe Lys Pro Ser Arg Val Ile Leu Gln
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 Asp Phe Thr Gly Val Pro Ala Val Val Asp Leu Ala Ser Leu Arg Lys
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 Pro Val Asp Leu Val Ile Asp His Ser Val Gln Val Asp Ser Tyr Ala
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 Asn Pro Asp Ala Leu Gln Arg Asn Met Lys Leu Glu Phe Glu Arg Asn

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Tyr	Glu	Arg	Tyr	Gln	Phe	Leu	Asn	Trp	Ala	Thr	Lys	Ala	Phe	Asp	Asn	
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Glu	Tyr	Leu	Ala	Asn	Val	Val	His	Val	Arg	Asp	Val	Asp	Gly	Glu	Gln	
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Thr	Ala	Phe	Pro	Asp	Thr	Leu	Val	Gly	Thr	Asp	Ser	His	Thr	Thr	Met	
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Glu	Ala	Gly	Met	Leu	Gly	Gln	Pro	Ser	Tyr	Phe	Pro	Ile	Pro	Glu	Val	
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Ala	Asp	Arg	Ala	Thr	Ile	Ala	Asn	Met	Ala	Pro	Glu	Tyr	Gly	Ala	Thr	
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Cys	Gly	Phe	Phe	Pro	Val	Asp	Glu	Glu	Ser	Leu	Lys	Tyr	Met	Lys	Leu	
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Thr	Gly	Arg	Lys	Asp	Asp	His	Ile	Ala	Leu	Val	Lys	Glu	Tyr	Leu	Gln	
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Gln	Asn	Asn	Met	Phe	Phe	Gln	Val	Glu	Asn	Glu	Asp	Pro	Glu	Tyr	Thr	
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Glu	Val	Ile	Asp	Leu	Asp	Leu	Ser	Thr	Val	Gln	Ala	Ser	Leu	Ser	Gly	
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Pro	Lys	Arg	Pro	Gln	Asp	Leu	Ile	Phe	Leu	Ser	Asp	Met	Lys	Thr	Glu	
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	Asp	Ser	Gly	Leu	Gln	Glu	Tyr	Leu	Asp	Asp	Leu	Gly	Phe	Asn	Leu	Val	
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	Val	Ala	Asp	Thr	Val	Asp	Ser	Val	Val	Thr	Pro	Glu	Leu	Phe	Leu	Glu	
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	Glu	Tyr	Ala	Asn	Val	Tyr	Glu	Asn	Asn	Glu	Met	Trp	Asn	Glu	Ile	Asp	
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 <213> Corynebacterium thermoaminogenes

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Ser	Val	Leu	Arg	Gln	Glu	Asp	Asp	Phe	Val	Ile	Thr	Asp	Asp	His	Ile	
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His	Val	Arg	Asp	Val	Asp	Gly	Glu	Gln	Thr	Ala	Phe	Pro	Asp	Thr	Leu	
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Pro	Ser	Tyr	Phe	Pro	Ile	Pro	Glu	Val	Ile	Gly	Val	Lys	Leu	Ser	Asn	
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Glu	Leu	Pro	Gln	Gly	Ser	Thr	Ala	Thr	Asp	Leu	Ala	Leu	Arg	Val	Thr	
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Glu	Glu	Leu	Arg	Lys	Arg	Gly	Val	Val	Gly	Lys	Phe	Val	Glu	Phe	Phe	
		275					280					285				
Gly	Pro	Gly	Val	Thr	Asn	Leu	Pro	Leu	Ala	Asp	Arg	Ala	Thr	Ile	Ala	
	290					295					300					
Asn	Met	Ala	Pro	Glu	Tyr	Gly	Ala	Thr	Cys	Gly	Phe	Phe	Pro	Val	Asp	
305					310					315					320	
Glu	Glu	Ser	Leu	Lys	Tyr	Met	Lys	Leu	Thr	Gly	Arg	Lys	Asp	Asp	His	
				325					330					335		
Ile	Ala	Leu	Val	Lys	Glu	Tyr	Leu	Gln	Gln	Asn	Asn	Met	Phe	Phe	Gln	
			340					345					350			
Val	Glu	Asn	Glu	Asp	Pro	Glu	Tyr	Thr	Glu	Val	Ile	Asp	Leu	Asp	Leu	
		355					360					365				

Ser	Thr	Val	Gln	Ala	Ser	Leu	Ser	Gly	Pro	Lys	Arg	Pro	Gln	Asp	Leu
	370					375					380				
Ile	Phe	Leu	Ser	Asp	Met	Lys	Thr	Glu	Phe	Glu	Lys	Ser	Val	Thr	Ala
385					390					395					400
Pro	Ala	Gly	Asn	Gln	Gly	His	Gly	Leu	Asp	Glu	Ser	Glu	Phe	Asp	Lys
				405					410					415	
Lys	Ala	Glu	Ile	Lys	Phe	Asn	Asp	Gly	Arg	Thr	Ser	Thr	Met	Lys	Thr
			420					425					430		
Gly	Asp	Val	Ala	Ile	Ala	Ala	Ile	Thr	Ser	Cys	Thr	Asn	Thr	Ser	Asn
		435					440					445			
Pro	Tyr	Val	Met	Leu	Gly	Ala	Gly	Leu	Val	Ala	Lys	Lys	Ala	Ile	Glu
	450					455					460				
Lys	Gly	Leu	Lys	Val	Pro	Asp	Tyr	Val	Lys	Thr	Ser	Leu	Ala	Pro	Gly
465					470					475					480
Ser	Lys	Val	Val	Thr	Gly	Tyr	Leu	Arg	Asp	Ser	Gly	Leu	Gln	Glu	Tyr
				485					490					495	
Leu	Asp	Asp	Leu	Gly	Phe	Asn	Leu	Val	Gly	Tyr	Gly	Cys	Thr	Thr	Cys
			500					505					510		
Ile	Gly	Asn	Ser	Gly	Pro	Leu	Leu	Pro	Glu	Ile	Glu	Lys	Ala	Val	Ala
		515					520					525			
Asp	Glu	Asp	Leu	Leu	Val	Thr	Ser	Val	Leu	Ser	Gly	Asn	Arg	Asn	Phe
	530					535					540				
Glu	Gly	Arg	Ile	His	Pro	Leu	Val	Lys	Ala	Asn	Tyr	Leu	Ala	Ser	Pro
545					550					555					560
Gln	Leu	Val	Val	Ala	Tyr	Ala	Leu	Ala	Gly	Thr	Val	Asp	Ile	Asp	Leu
				565					570					575	
His	Asn	Glu	Pro	Ile	Gly	Lys	Gly	Lys	Asp	Gly	Glu	Asp	Val	Tyr	Leu
			580					585					590		
Lys	Asp	Ile	Trp	Pro	Ser	Ile	Lys	Glu	Val	Ala	Asp	Thr	Val	Asp	Ser
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Val	Val	Thr	Pro	Glu	Leu	Phe	Leu	Glu	Glu	Tyr	Ala	Asn	Val	Tyr	Glu
	610					615					620				
Asn	Asn	Glu	Met	Trp	Asn	Glu	Ile	Asp	Val	Thr	Asp	Ala	Pro	Leu	Tyr
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Asp	Phe	Asp	Pro	Asn	Ser	Thr	Tyr	Ile	Gln	Asn	Pro	Ser	Phe	Phe	Gln
				645					650					655	
Gly	Leu	Ser	Lys	Glu	Pro	Gly	Thr	Ile	Glu	Pro	Leu	Lys	Asp	Leu	Arg
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Ile	Met	Gly	Lys	Phe	Gly	Asp	Ser	Val	Thr	Thr	Asp	His	Ile	Ser	Pro
		675				680						685			
Ala	Gly	Ala	Ile	Gly	Lys	Asp	Thr	Pro	Ala	Gly	Lys	Tyr	Leu	Leu	Asp
	690					695					700				
His	Asp	Val	Pro	Ile	Arg	Glu	Phe	Asn	Ser	Tyr	Gly	Ser	Arg	Arg	Gly
705					710					715					720
Asn	His	Glu	Val	Met	Val	Arg	Gly	Thr	Phe	Ala	Asn	Ile	Arg	Ile	Lys
				725					730					735	
Asn	Gln	Leu	Ala	Pro	Gly	Thr	Glu	Gly	Gly	Phe	Thr	Thr	Tyr	Trp	Pro
			740					745					750		
Thr	Glu	Glu	Ile	Met	Pro	Ile	Tyr	Asp	Ala	Ala	Met	Arg	Tyr	Lys	Glu
	755						760					765			
Asn	Gly	Thr	Gly	Leu	Ala	Val	Leu	Ala	Gly	Asn	Asp	Tyr	Gly	Met	Gly

770 775 780
 Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr Asn Leu Leu Gly Val Lys
 785 790 795 800
 Thr Val Ile Ala Gln Ser Tyr Glu Arg Ile His Arg Ser Asn Leu Val
 805 810 815
 Met Met Gly Val Leu Pro Leu Gln Phe Lys Gln Gly Glu Ser Ala Asp
 820 825 830
 Ser Leu Gly Leu Glu Gly Lys Glu Glu Ile Ser Val Asp Ile Asp Glu
 835 840 845
 Asn Val Lys Pro His Asp Leu Val Thr Val His Ala Lys Lys Glu Asn
 850 855 860
 Gly Glu Val Val Asp Phe Glu Ala Met Val Arg Phe Asp Ser Leu Val
 865 870 875 880
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 885 890 895
 Asn Lys Leu Ala Gln
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<210> 29
 <211> 3006
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>
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 atcgccgggg agagcagcat ggtcacacgc ctgcggcgtg ccctgggtgaa ggatcacggc 180
 ctggacagat cgcaggtggc attcatgggt tattggaggc agggagtggc catgaggggt 240
 tgatatcgct tccctgaggg tccgcaggcg tgcctcacc tgtattcttg atagttgaac 300
 aaaagagccc acataacaag gagactc atg gct aag atc atc tgg acc cgc acc 354
 Met Ala Lys Ile Ile Trp Thr Arg Thr
 1 5
 gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag ccg gtc gtc gag 402
 Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys Pro Val Val Glu 25
 10 15 20
 gct ttc gcc gcc acc gcg ggc atc gag gtg gag acc cgc gat atc tct 450
 Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr Arg Asp Ile Ser 40
 30 35 40
 ctc gcc ggt cgc atc ctc gca cag ttc gcg gac cag ctc ccc gag gag 498
 Leu Ala Gly Arg Ile Leu Ala Gln Phe Ala Asp Gln Leu Pro Glu Glu 55
 45 50 55
 cag aag gtc tcc gac gcc ctc gcc gag ctc ggc gaa ctg gct aag acc 546
 Gln Lys Val Ser Asp Ala Leu Ala Glu Leu Gly Glu Leu Ala Lys Thr 70
 60 65 70
 ccc gaa gcc aac atc atc aag ctt ccc aac atc tcc gca tcc gta ccg 594
 Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser Ala Ser Val Pro 85
 75 80

cag ctc aag gct gcc gta aag gaa ctg cag gaa cag ggc tac gac ctg	642
Gln Leu Lys Ala Ala Val Lys Glu Leu Gln Glu Gln Gly Tyr Asp Leu	100 105
90 95	
ccc gag tac gag gat gcc aag gac cgc tac gcc gct gtc atc ggc tcc	690
Pro Glu Tyr Glu Asp Ala Lys Asp Arg Tyr Ala Ala Val Ile Gly Ser	110 115 120
aac gtc aac ccg gtc ctg cgc gag ggc aac tcc gac cgc cgc gca ccg	738
Asn Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro	125 130 135
gtg gcc gtg aag aac ttc gtg aag aag ttc ccc cac cgc atg ggc gag	786
Val Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu	140 145 150
tgg tcc gcc gac tcc aag acc aac gtt gcc acc atg ggt gcc gac gac	834
Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Gly Ala Asp Asp	155 160 165
ttc cgc agc aat gag aag tcc gtg atc atg gac gag gcc gac acc gtg	882
Phe Arg Ser Asn Glu Lys Ser Val Ile Met Asp Glu Ala Asp Thr Val	170 175 180 185
gtg atc aag cat gtc gcc gcc gac ggc acc gag acc gtg ctc aag gac	930
Val Ile Lys His Val Ala Ala Asp Gly Thr Glu Thr Val Leu Lys Asp	190 195 200
agc ctc ccc ctg ctc aag ggt gag gtc atc gac ggc acc ttc atc tcc	978
Ser Leu Pro Leu Leu Lys Gly Glu Val Ile Asp Gly Thr Phe Ile Ser	205 210 215
gcc aag gca ctg gac gcc ttc ctg ctc gac cag gtc aaa cgc gcc aag	1026
Ala Lys Ala Leu Asp Ala Phe Leu Leu Asp Gln Val Lys Arg Ala Lys	220 225 230
gag gag ggc atc ctc ttc tcc gcc cac atg aag gcc acc atg atg aag	1074
Glu Glu Gly Ile Leu Phe Ser Ala His Met Lys Ala Thr Met Met Lys	235 240 245
gtc tcc gac ccg atc atc ttc ggc cac atc gtc cgc gcc tac ttc gcc	1122
Val Ser Asp Pro Ile Ile Phe Gly His Ile Val Arg Ala Tyr Phe Ala	250 255 260 265
gat gtc tac gca cag tac ggt gag cag ctg ctc gcc gcc ggc ctc aac	1170
Asp Val Tyr Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly Leu Asn	270 275 280
ggt gag aac ggt ctc gcc gcc atc tac gcc ggc ctg gac aag ctg gac	1218
Gly Glu Asn Gly Leu Ala Ala Ile Tyr Ala Gly Leu Asp Lys Leu Asp	285 290 295
aac ggt gcc gag atc aag gca gcc ttc gac aag ggc ctg gaa gag ggc	1266
Asn Gly Ala Glu Ile Lys Ala Ala Phe Asp Lys Gly Leu Glu Glu Gly	300 305 310
ccc gac ctg gcc atg gtg aac tcc gcc aag ggc atc acc aac ctg cat	1314
Pro Asp Leu Ala Met Val Asn Ser Ala Lys Gly Ile Thr Asn Leu His	315 320 325
gtg ccc tcc gat gtc atc atc gac gcc tcc atg ccc gcc atg atc cgc	1362
Val Pro Ser Asp Val Ile Ile Asp Ala Ser Met Pro Ala Met Ile Arg	330 335 340 345
acc tcc ggc aag atg tgg aac aag gac gac cag acc cag gat gcc ctg	1410
Thr Ser Gly Lys Met Trp Asn Lys Asp Asp Gln Thr Gln Asp Ala Leu	350 355 360

gct gtc atc ccg gac tcc tcc tac gcc ggt gtc tac cag acc gtc atc	1458
Ala Val Ile Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr Val Ile	
365 370 375	
gag gac tgc cgc aag aat ggc gcc ttc gat ccg acc acc atg ggc acc	1506
Glu Asp Cys Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met Gly Thr	
380 385 390	
gtc ccc aac gtc ggt ctg atg gca cag aag gcc gag gag tac ggc tcc	1554
Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr Gly Ser	
395 400 405	
cac gac aag acc ttc cgt atc gag gcc gac ggc aag gta cag gtc gtc	1602
His Asp Lys Thr Phe Arg Ile Glu Ala Asp Gly Lys Val Gln Val Val	
410 415 420 425	
gcc tcc aac ggt gat gtc ctc atc gag cac gac gtg gag aag ggc gac	1650
Ala Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Lys Gly Asp	
430 435 440	
atc tgg cgc gcc tgc cag acc aag gac gcc ccg atc cag gac tgg gtc	1698
Ile Trp Arg Ala Cys Gln Thr Lys Asp Ala Pro Ile Gln Asp Trp Val	
445 450 455	
aag ctg gct gtc aac cgc gca cgt ctc tcc ggc atg ccc gct gtg ttc	1746
Lys Leu Ala Val Asn Arg Ala Arg Leu Ser Gly Met Pro Ala Val Phe	
460 465 470	
tgg ctg gat ccc gcc cgc gca cac gac cgc aac ctg acc aca ctg gtg	1794
Trp Leu Asp Pro Ala Arg Ala His Asp Arg Asn Leu Thr Thr Leu Val	
475 480 485	
gag aag tac ctg gca gac cac gac acc gag ggc ctg gac atc cag atc	1842
Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile	
490 495 500 505	
ctc tcc ccc gtc gag gcc acc cag cac gcc atc gac cgc atc cgc cgc	1890
Leu Ser Pro Val Glu Ala Thr Gln His Ala Ile Asp Arg Ile Arg Arg	
510 515 520	
ggc gag gac acc atc tcc gtc acc ggt aac gtc ctg cgt gac tac aac	1938
Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp Tyr Asn	
525 530 535	
acc gac ctc ttc ccg atc ctc gag ctg ggc acc tcc gcc aag atg ctc	1986
Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys Met Leu	
540 545 550	
tcc gtc gtg cca ctg atg gcc ggc ggt gga ctc ttc gag acc ggt gcc	2034
Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala	
555 560 565	
ggt ggc tcc gcc ccg aag cac gtc cag cag gtc atc gag gaa aac cac	2082
Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Ile Glu Glu Asn His	
570 575 580 585	
ctg cgc tgg gat tcc ctc ggt gag ttc ctg gcc gag tcc ttc	2130
Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe	
590 595 600	
cgc cac gag ctc aac acc cgc aac aac acc aag gcc ggt gtc ctc gcc	2178
Arg His Glu Leu Asn Thr Arg Asn Asn Thr Lys Ala Gly Val Leu Ala	
605 610 615	
gat gcc ctg gac cgt gcg acc gag aag ctc ctc aac gag gag aag tcc	2226
Asp Ala Leu Asp Arg Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser	
620 625 630	

ccg tcc cgc aag gtc ggc gag atc gac aac cgt ggt tcc cac ttc tgg 2274
 Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp
 635 640
 ctg gcc acc tac tgg gcc gat gaa ctg gcc aac cag acc gag gac gcc 2322
 Leu Ala Thr Tyr Trp Ala Asp Glu Leu Ala Asn Gln Thr Glu Asp Ala
 650 655 660
 gag ctg gct gag acc ttc gcc cct gtc gcc gag gcc ctg aac aac cag 2370
 Glu Leu Ala Glu Thr Phe Ala Pro Val Ala Glu Ala Leu Asn Asn Gln
 670 675 680
 gct gcc gac atc gac gca gca ctc atc ggt gag cag ggc aag cct gtc 2418
 Ala Ala Asp Ile Asp Ala Ala Leu Ile Gly Glu Gln Gly Lys Pro Val
 685 690 695
 gac ctg ggt ggc tac tac gca ccc tcc gat gag aag acc tcc gcg atc 2466
 Asp Leu Gly Tyr Tyr Ala Pro Ser Asp Glu Lys Thr Ser Ala Ile
 700 705 710
 atg cgc ccg gtg gcc gca ttc aac gag atc atc gac tcc ctg aag aag 2514
 Met Arg Pro Val Ala Ala Phe Asn Glu Ile Ile Asp Ser Leu Lys Lys
 715 720 725
 taaccccttc tccggagccg acagccgacg gccacgctcc cccgcccacg ggggatcgtg 2574
 gccgtcggcc gtttctggca ctggagtga cacttcggtg ataatggtga gatgaacagc 2634
 ccccggtgcc ccgccatcct gtccgccggt tccgccgtgg gtctgatcgc tgcgctgggc 2694
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<211> 729

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 30

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 Ile Glu Val Glu Thr Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala
 35 40 45
 Gln Phe Ala Asp Gln Leu Pro Glu Glu Gln Lys Val Ser Asp Ala Leu
 50 55 60
 Ala Glu Leu Gly Glu Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys
 65 70 75 80
 Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Val Lys
 85 90 95
 Glu Leu Gln Glu Gln Gly Tyr Asp Leu Pro Glu Tyr Glu Asp Ala Lys
 100 105 110
 Asp Arg Tyr Ala Ala Val Ile Gly Ser Asn Val Asn Pro Val Leu Arg
 115 120 125
 Glu Gly Asn Ser Asp Arg Arg Ala Pro Val Ala Val Lys Asn Phe Val

130 135 140
 Lys Lys Phe Pro His Arg Met Gly Glu Trp Ser Ala Asp Ser Lys Thr
 145 150 155
 Asn Val Ala Thr Met Gly Ala Asp Asp Phe Arg Ser Asn Glu Lys Ser
 165 170 175
 Val Ile Met Asp Glu Ala Asp Thr Val Val Ile Lys His Val Ala Ala
 180 185 190
 Asp Gly Thr Glu Thr Val Leu Lys Asp Ser Leu Pro Leu Leu Lys Gly
 195 200 205
 Glu Val Ile Asp Gly Thr Phe Ile Ser Ala Lys Ala Leu Asp Ala Phe
 210 215 220
 Leu Leu Asp Gln Val Lys Arg Ala Lys Glu Glu Gly Ile Leu Phe Ser
 225 230 235 240
 Ala His Met Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe
 245 250 255
 Gly His Ile Val Arg Ala Tyr Phe Ala Asp Val Tyr Ala Gln Tyr Gly
 260 265 270
 Glu Gln Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala
 275 280 285
 Ile Tyr Ala Gly Leu Asp Lys Leu Asp Asn Gly Ala Glu Ile Lys Ala
 290 295 300
 Ala Phe Asp Lys Gly Leu Glu Glu Gly Pro Asp Leu Ala Met Val Asn
 305 310 315 320
 Ser Ala Lys Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Ile
 325 330 335
 Asp Ala Ser Met Pro Ala Met Ile Arg Thr Ser Gly Lys Met Trp Asn
 340 345 350
 Lys Asp Asp Gln Thr Gln Asp Ala Leu Ala Val Ile Pro Asp Ser Ser
 355 360 365
 Tyr Ala Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly
 370 375 380
 Ala Phe Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met
 385 390 395 400
 Ala Gln Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile
 405 410 415
 Glu Ala Asp Gly Lys Val Gln Val Val Ala Ser Asn Gly Asp Val Leu
 420 425 430
 Ile Glu His Asp Val Glu Lys Gly Asp Ile Trp Arg Ala Cys Gln Thr
 435 440 445
 Lys Asp Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Asn Arg Ala
 450 455 460
 Arg Leu Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Ala Arg Ala
 465 470 475 480
 His Asp Arg Asn Leu Thr Thr Leu Val Glu Lys Tyr Leu Ala Asp His
 485 490 495
 Asp Thr Glu Gly Leu Asp Ile Gln Ile Leu Ser Pro Val Glu Ala Thr
 500 505 510
 Gln His Ala Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val
 515 520 525
 Thr Gly Asn Val Leu Arg Asp Tyr Asn Thr Asp Leu Phe Pro Ile Leu
 530 535 540

Glu Leu Gly Thr Ser Ala Lys Met Leu Ser Val Val Pro Leu Met Ala
 545 550 555 560
 Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro Lys His
 565 570 575
 Val Gln Gln Val Ile Glu Glu Asn His Leu Arg Trp Asp Ser Leu Gly
 580 585 590
 Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn Thr Arg
 595 600 605
 Asn Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Arg Ala Thr
 610 615 620
 Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val Gly Glu
 625 630 635 640
 Ile Asp Asn Arg Gly Ser His Phe Trp Leu Ala Thr Tyr Trp Ala Asp
 645 650 655
 Glu Leu Ala Asn Gln Thr Glu Asp Ala Glu Leu Ala Glu Thr Phe Ala
 660 665 670
 Pro Val Ala Glu Ala Leu Asn Asn Gln Ala Ala Asp Ile Asp Ala Ala
 675 680 685
 Leu Ile Gly Glu Gln Gly Lys Pro Val Asp Leu Gly Gly Tyr Tyr Ala
 690 695 700
 Pro Ser Asp Glu Lys Thr Ser Ala Ile Met Arg Pro Val Ala Ala Phe
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 725

<210> 31
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 <212> DNA
 <213> *Corynebacterium thermoaminogenes*

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 <222> (806)..(2212)

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 cctagcctct gccgatgcta aaagtcagct gacccttgg ggcgcttcat ttgaaactgc 180
 gaccaagctc atgaatgcgc gaaagcattt ccattataag ggtaagctgt aagaatagtg 240
 ggagaaaatg ttcagtcgtg ttctaactca cttgagaaat tccatttttc tgggcttctc 300
 tcaaatagat taagtggccc gtatgctgga tttctagaat atttagaagc gcgccaactc 360
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 gagcgttaga agctttgtag agtgctcatt ccttgctgac ggcaagggtt tcctaccatg 480
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 cttgaacaga tcatcttctt catcaacacc atcttgggtt atggtctgca cgctggttct 600
 tccgcttcca gcaacctttc tcacacgata ggctgttctt aggcctaatt ggtaataagg 660
 ctgtgtaaca gtcgcccgcg tgattgtgtc ttttttaggcg cccgcgcggg cgattttcgg 720
 ttttcatctt ttttaaattg agtttggaag atcaagtgcc cccggatgca cgacaatgct 780
 atgccgaaca cgtattgttg aaatc gtg act gaa cat tat gac gta gta gta 832
 Val Thr Glu His Tyr Asp Val Val Val

ctc	gga	gct	ggc	ccc	ggt	ggc	tat	gtc	tcc	gcc	atc	cgc	gcc	gcg	cag	880
Leu	Gly	Ala	Gly	Pro	Gly	Gly	Tyr	Val	Ser	Ala	Ile	Arg	Ala	Ala	Gln	
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ctc	ggt	aag	aaa	gtt	gcg	gtt	atc	gag	aag	cag	tac	tgg	gga	ggt	gtc	928
Leu	Gly	Lys	Lys	Val	Ala	Val	Ile	Glu	Lys	Gln	Tyr	Trp	Gly	Gly	Val	
				30					35					40		
tgc	ctg	aat	gtg	ggt	tgt	atc	cca	tct	aag	gcg	ttg	atc	aag	aac	gct	976
Cys	Leu	Asn	Val	Gly	Cys	Ile	Pro	Ser	Lys	Ala	Leu	Ile	Lys	Asn	Ala	
			45					50					55			
gag	atc	gcc	cac	atc	ttc	aac	cat	gag	aag	aag	acc	ttc	ggc	atc	aac	1024
Glu	Ile	Ala	His	Ile	Phe	Asn	His	Glu	Lys	Lys	Thr	Phe	Gly	Ile	Asn	
		60					65					70				
ggc	gag	gtc	acc	ttc	aac	tac	gag	gat	gcc	cac	aag	cgt	tcc	cgt	ggt	1072
Gly	Glu	Val	Thr	Phe	Asn	Tyr	Glu	Asp	Ala	His	Lys	Arg	Ser	Arg	Gly	
	75				80						85					
gtc	tcc	gac	aag	atc	gtc	ggc	ggt	gtt	cac	tac	ttg	atg	aag	aag	aac	1120
Val	Ser	Asp	Lys	Ile	Val	Gly	Gly	Val	His	Tyr	Leu	Met	Lys	Lys	Asn	
90					95					100					105	
aag	atc	acc	gag	atc	gac	ggt	ttc	ggc	acc	ttc	aag	gat	gcc	aag	acc	1168
Lys	Ile	Thr	Glu	Ile	Asp	Gly	Phe	Gly	Thr	Phe	Lys	Asp	Ala	Lys	Thr	
				110					115					120		
atc	gag	gtg	acc	gat	ggt	aag	gat	gcc	ggc	aag	acc	gtc	acc	ttc	gat	1216
Ile	Glu	Val	Thr	Asp	Gly	Lys	Asp	Ala	Gly	Lys	Thr	Val	Thr	Phe	Asp	
			125					130					135			
gac	tgc	atc	atc	gcc	acc	ggt	tcc	gtg	gtc	aac	tcc	ctc	cgt	ggt	gtt	1264
Asp	Cys	Ile	Ile	Ala	Thr	Gly	Ser	Val	Val	Asn	Ser	Leu	Arg	Gly	Val	
		140					145					150				
gag	ttc	tcc	gag	aac	gtg	gtc	tcc	tac	gag	gag	cag	atc	ctc	aac	ccg	1312
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gtg	gcg	cct	aag	aag	atg	gtc	atc	gtc	ggt	ggc	ggc	gcc	atc	ggt	atg	1360
Val	Ala	Pro	Lys	Lys	Met	Val	Ile	Val	Gly	Gly	Gly	Ala	Ile	Gly	Met	
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Glu	Phe	Met	Asp	Arg	Val	Leu	Pro	Asn	Glu	Asp	Pro	Glu	Val	Ser	Lys	
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gtt	atc	gcc	aag	gcc	tac	aag	aag	atg	ggc	atc	aag	ctc	ctc	ccg	ggc	1504
Val	Ile	Ala	Lys	Ala	Tyr	Lys	Lys	Met	Gly	Ile	Lys	Leu	Leu	Pro	Gly	
		220					225					230				
cac	gca	acc	acc	gcg	gtg	cgc	gac	aat	ggc	gat	tcc	gtt	gag	gtc	gat	1552
His	Ala	Thr	Thr	Ala	Val	Arg	Asp	Asn	Gly	Asp	Ser	Val	Glu	Val	Asp	
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tac	cag	aag	aag	ggc	tcg	gac	aag	acc	gag	acc	atc	acc	gtc	gac	cgt	1600
Tyr	Gln	Lys	Lys	Gly	Ser	Asp	Lys	Thr	Glu	Thr	Ile	Thr	Val	Asp	Arg	
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Val	Leu	Ile	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	
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Glu His Met Arg Thr Asn Val Asp Gly Ile Tyr Ala Ile Gly Asp Val	
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Thr Ala Lys Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Ile Val	
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Ala Ala Glu Thr Leu Ala Gly Ala Glu Thr Gln Thr Leu Gly Asp Tyr	
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Gly Tyr Thr Glu Glu Gln Ala Lys Glu Lys Trp Pro Asp Arg Glu Ile	
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Lys Val Ser Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu	
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Ala Glu Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly	
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Glu Leu Leu Gly Gly His Ile Val Gly Ala Asn Ala Ser Glu Leu Leu	
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Asn Glu Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile	
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<212> PRT

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Ser	Tyr	Glu	Glu	Gln	Ile	Leu	Asn	Pro	Val	Ala	Pro	Lys	Lys	Met	Val
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Ile	Val	Gly	Gly	Gly	Ala	Ile	Gly	Met	Glu	Phe	Ala	Tyr	Val	Leu	Gly
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Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu	Thr	Asp	Gly	Phe	Ala
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Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu	Leu	Gly	Gly	His	Ile
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Val	Gly	Ala	Asn	Ala	Ser	Glu	Leu	Leu	Asn	Glu	Leu	Val	Leu	Ala	Gln
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455

460

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Glu Trp Arg Glu Leu Phe Glu Ser Gln Gly Gly Pro Gln Ala Glu Lys
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Ala Thr Pro Ala Thr Pro Glu Ala Lys Lys Ala Ala Ser Ser Gln Ser
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Ser Thr Ser Gly Gln Ser Thr Ala Lys Ala Ala Pro Ala Ala Lys Thr
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Ala Pro Ala Ser Ala Pro Ala Lys Ala Ala Pro Val Lys Gln Asn Gln
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gcg tcc aag cct gcc aag aag gcc aag gag tcc ccc ctg tcc aag cca 579
Ala Ser Lys Pro Ala Lys Lys Ala Lys Glu Ser Pro Leu Ser Lys Pro
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Ala Ala Met Pro Glu Pro Gly Thr Thr Pro Leu Arg Gly Ile Phe Lys
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tcc atc gcc aag aac atg gac ctc tcc ctc gag gtg ccc acc gcc acc 675
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Ser Val Arg Asp Met Pro Ala Arg Leu Met Phe Glu Asn Arg Ala Met
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Pro	Glu	His	Ile	Asn	Leu	Gly	Leu	Ala	Ile	Asp	Leu	Pro	Gln	Lys	Asp	
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Gly	Ser	Arg	Ala	Leu	Val	Val	Ala	Ala	Ile	Lys	Glu	Thr	Glu	Lys	Met	
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Thr	Phe	Ser	Gln	Phe	Leu	Glu	Ala	Tyr	Glu	Asp	Val	Val	Ala	Arg	Ser	
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cgc	gtc	ggc	aag	ctc	acc	atg	gat	gac	tac	cag	ggt	gtc	acc	atc	tcc	1059
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Thr	Pro	Met	Arg	Trp	Ala	Gln	Asp	Leu	Pro	Asn	Thr	Gly	Val	Asp	Lys	
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Asn	Thr	Arg	Val	Met	Gln	Leu	Ile	Glu	Ala	Tyr	Arg	Ser	Arg	Gly	His	
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Leu	Ile	Ala	Asp	Thr	Asn	Pro	Leu	Pro	Trp	Val	Gln	Pro	Gly	Met	Pro	
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Val	Pro	Asp	His	Arg	Asp	Leu	Asp	Ile	Glu	Thr	His	Gly	Leu	Thr	Leu	
415					420					425					430	
tgg	gat	ctg	gac	cgt	acc	ttc	cac	gtc	ggt	ggt	ttc	ggt	ggc	aag	gag	1587
Trp	Asp	Leu	Asp	Arg	Thr	Phe	His	Val	Gly	Gly	Phe	Gly	Gly	Lys	Glu	
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Leu	Lys	Val	Gly	Ser	Glu	Tyr	Thr	His	Ile	Leu	Asp	Arg	Asp	Glu	Arg	
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Thr	Trp	Leu	Gln	Asp	Arg	Leu	Glu	Ala	Gly	Met	Pro	Lys	Pro	Thr	Ala	
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Glu	Gly	Ala	Glu	Ser	Leu	Ile	Pro	Leu	Met	Asp	Ser	Ala	Ile	Asp	Thr	
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His	Leu	Glu	Ala	Val	Asn	Pro	Val	Val	Glu	Gly	Ile	Val	Arg	Ala	Lys	
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Gln	Asp	Ile	Leu	Asp	Lys	Gly	Pro	Asp	Gly	Tyr	Thr	Val	Val	Pro	Leu	
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Glu	Gln	Thr	Gly	Ile	Thr	Gly	Ser	Gln	Glu	Leu	Thr	Arg	Gly	Leu	Asp	
				835					840					845		
acc	aac	atc	acc	cgc	gag	gaa	ctg	gtc	gaa	ctc	ggc	cag	gcc	ttc	gtc	2835
Thr	Asn	Ile	Thr	Arg	Glu	Glu	Leu	Val	Glu	Leu	Gly	Gln	Ala	Phe	Val	
			850					855					860			
aac	acc	cca	gag	ggc	ttc	acc	tac	cac	cca	cgt	gtg	gca	ccg	gtg	gcc	2883
Asn	Thr	Pro	Glu	Gly	Phe	Thr	Tyr	His	Pro	Arg	Val	Ala	Pro	Val	Ala	
			865				870					875				
aag	aag	cgt	gcc	gag	tcc	gtc	acc	gag	ggt	ggc	atc	gac	tgg	gca	tgg	2931
Lys	Lys	Arg	Ala	Glu	Ser	Val	Thr	Glu	Gly	Gly	Ile	Asp	Trp	Ala	Trp	
880						885					890					
ggc	gag	ctc	atc	gcc	ttc	ggc	tcc	ctg	gcc	acc	tcc	ggc	agg	ctg	gtc	2979
Gly	Glu	Leu	Ile	Ala	Phe	Gly	Ser	Leu	Ala	Thr	Ser	Gly	Arg	Leu	Val	
895				900						905					910	
cgc	ctc	gcc	ggt	gag	gat	tcc	cgc	cgt	ggt	acc	ttc	acc	cag	cgt	cac	3027
Arg	Leu	Ala	Gly	Glu	Asp	Ser	Arg	Arg	Gly	Thr	Phe	Thr	Gln	Arg	His	
				915					920					925		
gcc	gtg	gcc	atc	gac	ccg	aac	acc	gcc	gag	gag	ttc	aac	ccg	ctc	cac	3075
Ala	Val	Ala	Ile	Asp	Pro	Asn	Thr	Ala	Glu	Glu	Phe	Asn	Pro	Leu	His	
			930					935					940			
gag	ctg	gca	cag	gcc	aag	ggc	ggc	ggc	aag	ttc	ctc	gtc	tac	aac	tcc	3123
Glu	Leu	Ala	Gln	Ala	Lys	Gly	Gly	Gly	Lys	Phe	Leu	Val	Tyr	Asn	Ser	
		945					950					955				
gcg	ctg	acc	gag	tac	gcg	ggt	atg	ggc	ttc	gaa	tac	ggc	tac	tcc	gtg	3171
Ala	Leu	Thr	Glu	Tyr	Ala	Gly	Met	Gly	Phe	Glu	Tyr	Gly	Tyr	Ser	Val	
		960				965					970					
ggc	aac	ccg	gac	gcc	gtg	gtg	tcc	tgg	gag	gca	cag	ttc	ggt	gac	ttc	3219
Gly	Asn	Pro	Asp	Ala	Val	Val	Ser	Trp	Glu	Ala	Gln	Phe	Gly	Asp	Phe	
975					980					985					990	

gcc aac ggt gca cag acc atc atc gat gag tac atc tcc tcc ggt gag 3267
Ala Asn Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser Ser Gly Glu
995 1000 1005
gcc aag tgg ggc cag acc tcc tcg gtc atc ctg ctg ctg ccc cac ggt 3315
Ala Lys Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu Pro His Gly
1010 1015 1020
tac gag ggc cag ggt ccg gac cac tcc tcc gca cgc atc gag cgt ttc 3363
Tyr Glu Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile Glu Arg Phe
1025 1030 1035
ctg cag ctg tgc gcc gag ggt tcc atg acc atc gcc cag ccg acc acc 3411
Leu Gln Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr Thr
1040 1045 1050
ccg gcg aac tac ttc cac ctg ctg cgt cgt cac gca ctg ggc aag atg 3459
Pro Ala Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly Lys Met
1055 1060 1065 1070
aag cgc ccg ctg gtc gtc ttc acc ccg aag tcc atg ctg cgc aac aag 3507
Lys Arg Pro Leu Val Phe Thr Pro Lys Ser Met Leu Arg Asn Lys
1075 1080 1085
gcc gcc acc tcc gct ccg gag gag ttc acc gag gtc acc cgc ttc aag 3555
Ala Ala Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr Arg Phe Lys
1090 1095 1100
tcc gtg atc gac gat ccg aac gtg gcg gat gcc tcc aag gtg aag aag 3603
Ser Val Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys Val Lys Lys
1105 1110 1115
atc atg ctg tgc tcc ggc aag atc tac tac gaa ctg gcc aag cgc aag 3651
Ile Met Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala Lys Arg Lys
1120 1125 1130
gag aag gac aac cgc gac gac atc gcg atc gtg cgc atc gag atg ctg 3699
Glu Lys Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile Glu Met Leu
1135 1140 1145 1150
cac ccg atc ccg ttc aac cgt ctg cgc gac gcc ttc gac ggc tac ccc 3747
His Pro Ile Pro Phe Asn Arg Leu Arg Asp Ala Phe Asp Gly Tyr Pro
1155 1160 1165
aac gcc gag gag atc ctg ttc gtt cag gac gag ccg gca aac cag ggt 3795
Asn Ala Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala Asn Gln Gly
1170 1175 1180
gcc tgg ccg ttc tac cag gag cac ctg ccc aac ctc atc gag ggc atg 3843
Ala Trp Pro Phe Tyr Gln Glu His Leu Pro Asn Leu Ile Glu Gly Met
1185 1190 1195
ctc ccg atg cgt cgc atc tcg cgc cgt tcc cag tcc tcg act gcg acc 3891
Leu Pro Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr
1200 1205 1210
ggt atc gcg aag gtg cac acc atc gag cag cag aag ctg ctg gat gat 3939
Gly Ile Ala Lys Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp
1215 1220 1225 1230
gcg ttc aac gca taaacgttaa tacagcggtt gataccttga accccgcccgc 3991
Ala Phe Asn Ala
acccttttaga tgcgggcggg gttttgcttt gcctgcatag gcgataatat tcatatacac 4051
ccatcacggtt taagttctgc atttgatcg tgcgagcatc ccggt 4096

<210> 34

<211> 1234

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 34

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Met	Phe	Gln	Gln	Phe	Lys	Lys	Asp	Pro	Gln	Ser	Val	Asp	Lys	Glu	Trp	
		20						25					30			
Arg	Glu	Leu	Phe	Glu	Ser	Gln	Gly	Gly	Pro	Gln	Ala	Glu	Lys	Ala	Thr	
		35					40					45				
Pro	Ala	Thr	Pro	Glu	Ala	Lys	Lys	Ala	Ala	Ser	Ser	Gln	Ser	Ser	Thr	
	50					55					60					
Ser	Gly	Gln	Ser	Thr	Ala	Lys	Ala	Ala	Pro	Ala	Ala	Lys	Thr	Ala	Pro	
65				70						75					80	
Ala	Ser	Ala	Pro	Ala	Lys	Ala	Ala	Pro	Val	Lys	Gln	Asn	Gln	Ala	Ser	
			85						90					95		
Lys	Pro	Ala	Lys	Lys	Ala	Lys	Glu	Ser	Pro	Leu	Ser	Lys	Pro	Ala	Ala	
			100					105					110			
Met	Pro	Glu	Pro	Gly	Thr	Thr	Pro	Leu	Arg	Gly	Ile	Phe	Lys	Ser	Ile	
		115					120					125				
Ala	Lys	Asn	Met	Asp	Leu	Ser	Leu	Glu	Val	Pro	Thr	Ala	Thr	Ser	Val	
	130					135					140					
Arg	Asp	Met	Pro	Ala	Arg	Leu	Met	Phe	Glu	Asn	Arg	Ala	Met	Val	Asn	
145					150					155					160	
Asp	Gln	Leu	Lys	Arg	Thr	Arg	Gly	Gly	Lys	Ile	Ser	Phe	Thr	His	Ile	
				165					170					175		
Ile	Gly	Tyr	Ala	Met	Val	Lys	Ala	Val	Met	Ala	His	Pro	Asp	Met	Asn	
			180					185					190			
Asn	Ser	Tyr	Asp	Ile	Val	Asp	Gly	Lys	Pro	Ser	Leu	Val	Val	Pro	Glu	
		195					200					205				
His	Ile	Asn	Leu	Gly	Leu	Ala	Ile	Asp	Leu	Pro	Gln	Lys	Asp	Gly	Ser	
	210					215					220					
Arg	Ala	Leu	Val	Val	Ala	Ala	Ile	Lys	Glu	Thr	Glu	Lys	Met	Thr	Phe	
225					230					235					240	
Ser	Gln	Phe	Leu	Glu	Ala	Tyr	Glu	Asp	Val	Val	Ala	Arg	Ser	Arg	Val	
				245					250					255		
Gly	Lys	Leu	Thr	Met	Asp	Asp	Tyr	Gln	Gly	Val	Thr	Ile	Ser	Leu	Thr	
			260					265					270			
Asn	Pro	Gly	Gly	Ile	Gly	Thr	Arg	His	Ser	Ile	Pro	Arg	Leu	Thr	Lys	
		275					280					285				
Gly	Gln	Gly	Thr	Ile	Ile	Gly	Val	Gly	Ser	Met	Asp	Tyr	Pro	Ala	Glu	
	290					295					300					
Phe	Gln	Gly	Ala	Ser	Glu	Asp	Arg	Leu	Ala	Glu	Leu	Gly	Val	Gly	Lys	
305					310					315					320	
Leu	Val	Thr	Ile	Thr	Ser	Thr	Tyr	Asp	His	Arg	Val	Ile	Gln	Gly	Ala	
				325					330					335		
Glu	Ser	Gly	Glu	Phe	Leu	Arg	Thr	Met	Ser	Gln	Leu	Leu	Val	Asp	Asp	
			340					345					350			
Ala	Phe	Trp	Asp	His	Ile	Phe	Glu	Glu	Met	Asn	Val	Pro	Tyr	Thr	Pro	
		355					360					365				

Met	Arg	Trp	Ala	Gln	Asp	Leu	Pro	Asn	Thr	Gly	Val	Asp	Lys	Asn	Thr
370						375					380				
Arg	Val	Met	Gln	Leu	Ile	Glu	Ala	Tyr	Arg	Ser	Arg	Gly	His	Leu	Ile
385					390					395					400
Ala	Asp	Thr	Asn	Pro	Leu	Pro	Trp	Val	Gln	Pro	Gly	Met	Pro	Val	Pro
				405					410					415	
Asp	His	Arg	Asp	Leu	Asp	Ile	Glu	Thr	His	Gly	Leu	Thr	Leu	Trp	Asp
			420					425					430		
Leu	Asp	Arg	Thr	Phe	His	Val	Gly	Gly	Phe	Gly	Gly	Lys	Glu	Thr	Met
	435						440					445			
Thr	Leu	Arg	Glu	Val	Leu	Ser	Arg	Leu	Arg	Ala	Ala	Tyr	Thr	Leu	Lys
	450					455					460				
Val	Gly	Ser	Glu	Tyr	Thr	His	Ile	Leu	Asp	Arg	Asp	Glu	Arg	Thr	Trp
465					470					475					480
Leu	Gln	Asp	Arg	Leu	Glu	Ala	Gly	Met	Pro	Lys	Pro	Thr	Ala	Ala	Glu
				485					490					495	
Gln	Lys	Tyr	Ile	Leu	Gln	Lys	Leu	Asn	Ala	Ala	Glu	Ala	Phe	Glu	Asn
			500					505					510		
Phe	Leu	Gln	Thr	Lys	Tyr	Val	Gly	Gln	Lys	Arg	Phe	Ser	Leu	Glu	Gly
	515						520					525			
Ala	Glu	Ser	Leu	Ile	Pro	Leu	Met	Asp	Ser	Ala	Ile	Asp	Thr	Ala	Ala
	530					535					540				
Gly	Gln	Gly	Leu	Asp	Glu	Val	Val	Ile	Gly	Met	Pro	His	Arg	Gly	Arg
545					550					555					560
Leu	Asn	Val	Leu	Phe	Asn	Ile	Val	Gly	Lys	Pro	Leu	Ala	Ser	Ile	Phe
				565					570					575	
Asn	Glu	Phe	Glu	Gly	Gln	Met	Glu	Gln	Gly	Gln	Ile	Gly	Gly	Ser	Gly
			580					585					590		
Asp	Val	Lys	Tyr	His	Leu	Gly	Ser	Glu	Gly	Thr	His	Leu	Gln	Met	Phe
	595						600					605			
Gly	Asp	Gly	Glu	Ile	Lys	Val	Ser	Leu	Thr	Ala	Asn	Pro	Ser	His	Leu
	610					615					620				
Glu	Ala	Val	Asn	Pro	Val	Val	Glu	Gly	Ile	Val	Arg	Ala	Lys	Gln	Asp
625					630					635					640
Ile	Leu	Asp	Lys	Gly	Pro	Asp	Gly	Tyr	Thr	Val	Val	Pro	Leu	Leu	Leu
				645					650					655	
His	Gly	Asp	Ala	Ala	Phe	Ala	Gly	Leu	Gly	Ile	Val	Pro	Glu	Thr	Ile
			660					665					670		
Asn	Leu	Ala	Ala	Leu	Arg	Gly	Tyr	Asp	Val	Gly	Gly	Thr	Ile	His	Ile
	675						680					685			
Val	Val	Asn	Asn	Gln	Ile	Gly	Phe	Thr	Thr	Thr	Pro	Asp	Ser	Ser	Arg
	690					695					700				
Ser	Met	His	Tyr	Ala	Thr	Asp	Cys	Ala	Lys	Ala	Phe	Gly	Cys	Pro	Val
705					710					715					720
Phe	His	Val	Asn	Gly	Asp	Asp	Pro	Glu	Ala	Val	Val	Trp	Val	Gly	Gln
				725					730					735	
Leu	Ala	Thr	Glu	Tyr	Arg	Arg	Arg	Phe	Gly	Lys	Asp	Val	Phe	Ile	Asp
			740					745					750		
Leu	Ile	Cys	Tyr	Arg	Leu	Arg	Gly	His	Asn	Glu	Ala	Asp	Asp	Pro	Ser
	755						760					765			
Met	Thr	Gln	Pro	Lys	Met	Tyr	Glu	Leu	Ile	Thr	Gly	Arg	Asp	Ser	Val

770	775	780
Arg Ala Thr Tyr Thr Glu Asp Leu Leu Gly Arg Gly Asp Leu Ser Pro		
785	790	795
Glu Asp Ala Glu Ala Val Val Arg Asp Phe His Asp Gln Met Glu Ser		800
	805	810
Val Phe Asn Glu Val Lys Glu Ala Gly Lys Lys Gln Pro Asp Glu Gln		815
	820	825
Thr Gly Ile Thr Gly Ser Gln Glu Leu Thr Arg Gly Leu Asp Thr Asn		830
	835	840
Ile Thr Arg Glu Glu Leu Val Glu Leu Gly Gln Ala Phe Val Asn Thr		845
	850	855
Pro Glu Gly Phe Thr Tyr His Pro Arg Val Ala Pro Val Ala Lys Lys		860
865	870	875
Arg Ala Glu Ser Val Thr Glu Gly Gly Ile Asp Trp Ala Trp Gly Glu		880
	885	890
Leu Ile Ala Phe Gly Ser Leu Ala Thr Ser Gly Arg Leu Val Arg Leu		895
	900	905
Ala Gly Glu Asp Ser Arg Arg Gly Thr Phe Thr Gln Arg His Ala Val		910
	915	920
Ala Ile Asp Pro Asn Thr Ala Glu Glu Phe Asn Pro Leu His Glu Leu		925
	930	935
Ala Gln Ala Lys Gly Gly Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu		940
945	950	955
Thr Glu Tyr Ala Gly Met Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn		960
	965	970
Pro Asp Ala Val Val Ser Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn		975
	980	985
Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser Ser Gly Glu Ala Lys		990
	995	1000
Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu Pro His Gly Tyr Glu		1005
	1010	1015
Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln		1020
1025	1030	1035
Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr Thr Pro Ala		1040
	1045	1050
Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly Lys Met Lys Arg		1055
	1060	1065
Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu Arg Asn Lys Ala Ala		1070
	1075	1080
Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr Arg Phe Lys Ser Val		1085
	1090	1095
Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys Val Lys Lys Ile Met		1100
1105	1110	1115
Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys		1120
	1125	1130
Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile Glu Met Leu His Pro		1135
	1140	1145
Ile Pro Phe Asn Arg Leu Arg Asp Ala Phe Asp Gly Tyr Pro Asn Ala		1150
	1155	1160
Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala Asn Gln Gly Ala Trp		1165
	1170	1175
		1180

Pro Phe Tyr Gln Glu His Leu Pro Asn Leu Ile Glu Gly Met Leu Pro
 1185 1190 1195 1200
 Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr Gly Ile
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 Asn Ala

<210> 35
 <211> 20
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: primer for aceA

<400> 35
 cctctaccca gcgaactccg 20

<210> 36
 <211> 20
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: primer for aceA

<400> 36
 ctgccttgaa ctcacgggtc 20

<210> 37
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence: primer for accBC

<400> 37
 catccacccc ggctacggct 20

<210> 38
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<220>
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<400> 38
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<210> 39
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 <223> Description of Artificial Sequence: primer for dtsR1

 <400> 39
 acggcccagc cctgaccgac 20

 <210> 40
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 <210> 41
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 <210> 42
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 <400> 42
 agcagcgccc atgacggcga 20

 <210> 43
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<223> Description of Artificial Sequence: primer for pfk
 <400> 43
 cgtcacccga ggaatcgtcc 20
 <210> 44
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 <220>
 <223> Description of Artificial Sequence: primer for pfk
 <400> 44
 cgtggcggcc catgacctcc 20
 <210> 45
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 <223> Description of Artificial Sequence: primer for scrB
 <220>
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 <222> (3)..(3)
 <223> n = a, c, g, or t
 <400> 45
 ggncghytba aygaycc 17
 <210> 46
 <211> 20
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 <223> Description of Artificial Sequence: primer for scrB
 <220>
 <221> misc_feature
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 <223> n = a, c, g, or t
 <400> 46
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 <210> 47
 <211> 20
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for gluABCD

<400> 47

ccatccggat ccggcaagtc

20

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for gluABCD

<400> 48

aatcccatct cgtgggtaac

20

<210> 49

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pdhA

<400> 49

actgtgtcca tgggtcttgg ccc

23

<210> 50

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pdhA

<400> 50

cgctggaatccgaacatcga

20

<210> 51

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pc

<400> 51

ggcgcaacct acgacgttgc aatgcg

26

<210> 52
 <211> 20
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 <220>
 <223> Description of Artificial Sequence: primer for pc

 <400> 52
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 <210> 53
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for ppc

 <400> 53
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 <210> 54
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for ppc

 <400> 54
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 <210> 55
 <211> 20
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 <220>
 <223> Description of Artificial Sequence: primer for acn

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 <220>
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 <223> n = inosine

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<220>
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<223> n = inosine

<400> 55
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<210> 56
<211> 20
<212> DNA
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<220>
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<400> 56
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<210> 57
<211> 20
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<220>
<223> Description of Artificial Sequence: primer for icd

<400> 57
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20

<210> 58
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<220>
 <223> Description of Artificial Sequence: primer for icd

 <400> 58
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 <210> 59
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 <220>
 <223> Description of Artificial Sequence: primer for lpd

 <400> 59
 atcatcgcaa ccggttc 17

 <210> 60
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 <220>
 <223> Description of Artificial Sequence: primer for lpd

 <400> 60
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 <210> 61
 <211> 20
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: primer for odhA

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 <210> 62
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 <220>
 <223> Description of Artificial Sequence: primer for odhA

 <400> 62
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 <210> 63

<211> 20
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 <220>
 <223> Description of Artificial Sequence: primer for
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 <400> 63
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 <210> 64
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 <220>
 <223> Description of Artificial Sequence: primer for
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 <400> 64
 ttgacgccgg tggtctccag 20

 <210> 65
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 <220>
 <223> Description of Artificial Sequence: primer for
 LA cloning of acn

 <400> 65
 ggtgaagcta agtagttagc 20

 <210> 66
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 <220>
 <223> Description of Artificial Sequence: primer for
 LA cloning of acn

 <400> 66
 agctactaaa cctgcacc 18

 <210> 67
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for
 LA cloning of icd

<400> 67
 ccgtactctt cagccttctg 20

<210> 68
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 LA cloning of icd

<400> 68
 tcgtccttgt tccacatc 18

<210> 69
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for
 LA cloning of lpd

<400> 69
 atcatcgcaa ccggttc 17

<210> 70
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for
 LA cloning of lpd

<400> 70
 tacgaggagc agatcctcaa 20

<210> 71
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for

LA cloning of acn

<400> 71
gctaactact tagcttcacc 20

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of acn

<400> 72
gaaccaggaa ctattgaacc 20

<210> 73
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 73
tccgatgtca tcatcgac 18

<210> 74
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 74
atgtggaaca aggacgac 18

<210> 75
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of odhA

<400> 75

gtacatatattg tcgttagaac gcgtaatacg actca 35

<210> 76
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for
 LA cloning of odhA

<400> 76
 cgttagaacg cgtaatacga ctcactatag ggaga 35

<210> 77
 <211> 32
 <212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer for
 amplifying gdh gene

<400> 77
 gcgcctgcag gtccgagggt gtgcgttcgg ca 32

<210> 78
 <211> 32
 <212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer for
 amplifying gdh gene

<400> 78
 gcgcctgcag ccaccagga tgccctcaacc ag 32

<210> 79
 <211> 1344
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>
 <221> CDS
 <222> (1)..(1341)

<400> 79

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Met	Thr	Val	Asp	Glu	Gln	Val	Ser	Asn	Tyr	Tyr	Asp	Met	Leu	Leu	Lys	
1				5					10					15		
cgc	aac	gcc	ggg	gaa	cct	gag	ttc	cac	cag	gct	gtc	gcg	gag	gtt	ctc	96
Arg	Asn	Ala	Gly	Glu	Pro	Glu	Phe	His	Gln	Ala	Val	Ala	Glu	Val	Leu	
		20					25					30				
gaa	tct	ctg	aag	atc	gtc	ctg	gag	aag	gac	ccg	cac	tac	gcc	gac	tac	144
Glu	Ser	Leu	Lys	Ile	Val	Leu	Glu	Lys	Asp	Pro	His	Tyr	Ala	Asp	Tyr	
		35				40					45					
ggg	ctg	atc	cag	cgt	ctc	tgc	gaa	ccg	gaa	cgc	cag	ctg	atc	ttc	cgt	192
Gly	Leu	Ile	Gln	Arg	Leu	Cys	Glu	Pro	Glu	Arg	Gln	Leu	Ile	Phe	Arg	
	50					55					60					
gtg	ccc	tgg	gtg	gat	gac	aac	ggg	cag	gtg	cac	gtc	aac	cgt	ggg	ttc	240
Val	Pro	Trp	Val	Asp	Asp	Asn	Gly	Gln	Val	His	Val	Asn	Arg	Gly	Phe	
	65				70					75					80	
cgt	gtc	cag	ttc	aac	tcc	gca	ctc	ggc	ccg	tac	aag	ggg	ggg	ctg	cgt	288
Arg	Val	Gln	Phe	Asn	Ser	Ala	Leu	Gly	Pro	Tyr	Lys	Gly	Gly	Leu	Arg	
				85					90				95			
ttc	cac	ccc	tcc	gtc	aac	ctc	ggc	atc	gtc	aag	ttc	ctc	ggc	ttc	gag	336
Phe	His	Pro	Ser	Val	Asn	Leu	Gly	Ile	Val	Lys	Phe	Leu	Gly	Phe	Glu	
			100				105						110			
cag	atc	ttc	aag	aac	tcc	ctc	acc	ggg	ctg	ccg	atc	ggg	ggc	ggc	aag	384
Gln	Ile	Phe	Lys	Asn	Ser	Leu	Thr	Gly	Leu	Pro	Ile	Gly	Gly	Gly	Lys	
		115					120					125				
ggg	ggg	tcc	gac	ttc	gac	ccg	aag	ggc	aag	tcc	gag	ctg	gag	atc	atg	432
Gly	Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Glu	Leu	Glu	Ile	Met	
	130					135					140					
cgc	ttc	tgc	cag	tcc	ttc	atg	acc	gag	ctg	cac	cgc	cac	atc	ggc	gag	480
Arg	Phe	Cys	Gln	Ser	Phe	Met	Thr	Glu	Leu	His	Arg	His	Ile	Gly	Glu	
					150					155					160	
tac	cgg	gat	gtc	ccg	gcc	ggg	gac	atc	gga	gtc	ggg	ggc	cgc	gag	atc	528
Tyr	Arg	Asp	Val	Pro	Ala	Gly	Asp	Ile	Gly	Val	Gly	Gly	Arg	Glu	Ile	
				165				170						175		
ggg	tac	ctc	ttc	ggc	cac	tac	cgc	cgt	ctg	gcc	aac	cag	cac	gag	tcc	576
Gly	Tyr	Leu	Phe	Gly	His	Tyr	Arg	Arg	Leu	Ala	Asn	Gln	His	Glu	Ser	
			180				185						190			
ggg	gtg	ctc	acc	ggc	aag	ggc	ctg	acc	tgg	ggg	ggg	tcc	ctg	gtc	cgc	624
Gly	Val	Leu	Thr	Gly	Lys	Gly	Leu	Thr	Trp	Gly	Gly	Ser	Leu	Val	Arg	
			195				200					205				
acc	gag	gcc	acc	ggc	ttc	ggc	acc	gtc	tac	ttc	gtc	cag	gag	atg	atc	672
Thr	Glu	Ala	Thr	Gly	Phe	Gly	Thr	Val	Tyr	Phe	Val	Gln	Glu	Met	Ile	
		210				215					220					
aag	gcg	gaa	ggg	gag	acc	ctc	gag	ggc	aag	aag	gtc	atc	gtc	tcc	ggg	720
Lys	Ala	Glu	Gly	Glu	Thr	Leu	Glu	Gly	Lys	Lys	Val	Ile	Val	Ser	Gly	
					230					235					240	
tcc	ggc	aac	gtg	gcc	acc	tac	gcc	atc	cag	aag	gtg	cag	gaa	ctg	ggg	768
Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Gln	Lys	Val	Gln	Glu	Leu	Gly	
				245					250					255		
gcg	gtt	gtg	gtc	ggc	ttc	tcc	gac	tcc	agc	ggc	tgg	gtc	tcc	acc	ccg	816
Ala	Val	Val	Val	Gly	Phe	Ser	Asp	Ser	Ser	Gly	Trp	Val	Ser	Thr	Pro	
			260				265						270			

aac ggt gtt gac gtg gcc aag ctg cgt gag atc aag gag gtc cgt cgt	864
Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg	
275 280 285	
gca cgc gtg tcc tcc tac gcc gac gag gtg gag ggt gcg gag tac cac	912
Ala Arg Val Ser Ser Tyr Ala Asp Glu Val Glu Gly Ala Glu Tyr His	
290 295 300	
acc gac ggc tcc atc tgg gat ctg acc gcc gac atc gcg ctg ccc tgc	960
Thr Asp Gly Ser Ile Trp Asp Leu Thr Ala Asp Ile Ala Leu Pro Cys	
305 310 315 320	
gcc acc cag aac gaa ctg gac ggc gac aac gcc cgc acc ctc gcg gac	1008
Ala Thr Gln Asn Glu Leu Asp Gly Asp Asn Ala Arg Thr Leu Ala Asp	
325 330 335	
aac ggc tgc cgc ttc gtg gcg gag ggc gcc aac atg ccc tcc acc ccc	1056
Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro	
340 345 350	
gag gcc atc gac gtc ttc cgt gag cgt ggt gtt ctc ttc ggg ccg ggc	1104
Glu Ala Ile Asp Val Phe Arg Glu Arg Gly Val Leu Phe Gly Pro Gly	
355 360 365	
aag gct gcc aac gcc ggt ggc gtg gcc acc tcc gcc ctg gag atg cag	1152
Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln	
370 375 380	
cag aac gcc tcc cgt gat tcc tgg agc ttc gag tac acc gat gag cgt	1200
Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg	
385 390 395 400	
ctc cac cgc atc atg aag aac atc ttc aag tcc tgc gcc gat acc gcc	1248
Leu His Arg Ile Met Lys Asn Ile Phe Lys Ser Cys Ala Asp Thr Ala	
405 410 415	
aag gag tac ggc cac gag aag aac tac gtg gtc ggt gcg aac atc gcc	1296
Lys Glu Tyr Gly His Glu Lys Asn Tyr Val Val Gly Ala Asn Ile Ala	
420 425 430	
gga ttc aag aag gtc gct gac gcc atg ctc gcc cag ggt gtc atc taa	1344
Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile	
435 440 445	

<210> 80

<211> 447

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 80

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Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu	
20 25 30	
Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr	
35 40 45	
Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg	
50 55 60	
Val Pro Trp Val Asp Asp Asn Gly Gln Val His Val Asn Arg Gly Phe	
65 70 75 80	
Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg	

				85				90					95		
Phe	His	Pro	Ser	Val	Asn	Leu	Gly	Ile	Val	Lys	Phe	Leu	Gly	Phe	Glu
			100					105					110		
Gln	Ile	Phe	Lys	Asn	Ser	Leu	Thr	Gly	Leu	Pro	Ile	Gly	Gly	Gly	Lys
		115					120					125			
Gly	Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Glu	Leu	Glu	Ile	Met
	130					135					140				
Arg	Phe	Cys	Gln	Ser	Phe	Met	Thr	Glu	Leu	His	Arg	His	Ile	Gly	Glu
145					150					155					160
Tyr	Arg	Asp	Val	Pro	Ala	Gly	Asp	Ile	Gly	Val	Gly	Gly	Arg	Glu	Ile
			165						170					175	
Gly	Tyr	Leu	Phe	Gly	His	Tyr	Arg	Arg	Leu	Ala	Asn	Gln	His	Glu	Ser
			180					185					190		
Gly	Val	Leu	Thr	Gly	Lys	Gly	Leu	Thr	Trp	Gly	Gly	Ser	Leu	Val	Arg
	195					200						205			
Thr	Glu	Ala	Thr	Gly	Phe	Gly	Thr	Val	Tyr	Phe	Val	Gln	Glu	Met	Ile
	210					215					220				
Lys	Ala	Glu	Gly	Glu	Thr	Leu	Glu	Gly	Lys	Lys	Val	Ile	Val	Ser	Gly
225					230					235					240
Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Gln	Lys	Val	Gln	Glu	Leu	Gly
			245						250					255	
Ala	Val	Val	Val	Gly	Phe	Ser	Asp	Ser	Ser	Gly	Trp	Val	Ser	Thr	Pro
			260					265					270		
Asn	Gly	Val	Asp	Val	Ala	Lys	Leu	Arg	Glu	Ile	Lys	Glu	Val	Arg	Arg
	275						280					285			
Ala	Arg	Val	Ser	Ser	Tyr	Ala	Asp	Glu	Val	Glu	Gly	Ala	Glu	Tyr	His
	290					295					300				
Thr	Asp	Gly	Ser	Ile	Trp	Asp	Leu	Thr	Ala	Asp	Ile	Ala	Leu	Pro	Cys
305					310					315					320
Ala	Thr	Gln	Asn	Glu	Leu	Asp	Gly	Asp	Asn	Ala	Arg	Thr	Leu	Ala	Asp
			325						330					335	
Asn	Gly	Cys	Arg	Phe	Val	Ala	Glu	Gly	Ala	Asn	Met	Pro	Ser	Thr	Pro
			340					345					350		
Glu	Ala	Ile	Asp	Val	Phe	Arg	Glu	Arg	Gly	Val	Leu	Phe	Gly	Pro	Gly
	355						360					365			
Lys	Ala	Ala	Asn	Ala	Gly	Gly	Val	Ala	Thr	Ser	Ala	Leu	Glu	Met	Gln
	370					375					380				
Gln	Asn	Ala	Ser	Arg	Asp	Ser	Trp	Ser	Phe	Glu	Tyr	Thr	Asp	Glu	Arg
385					390					395					400
Leu	His	Arg	Ile	Met	Lys	Asn	Ile	Phe	Lys	Ser	Cys	Ala	Asp	Thr	Ala
			405						410					415	
Lys	Glu	Tyr	Gly	His	Glu	Lys	Asn	Tyr	Val	Val	Gly	Ala	Asn	Ile	Ala
			420					425					430		
Gly	Phe	Lys	Lys	Val	Ala	Asp	Ala	Met	Leu	Ala	Gln	Gly	Val	Ile	
	435						440					445			

<210> 81

<211> 1344

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(1341)

<400> 81

atg	aca	gtt	gat	gag	cag	gtc	tct	aac	tat	tac	gac	atg	ctt	ctg	aag	48
Met	Thr	Val	Asp	Glu	Gln	Val	Ser	Asn	Tyr	Tyr	Asp	Met	Leu	Leu	Lys	
1				5				10					15			
cgc	aat	gct	ggc	gag	cct	gaa	ttt	cac	cag	gca	gtg	gca	gag	gtt	ttg	96
Arg	Asn	Ala	Gly	Glu	Pro	Glu	Phe	His	Gln	Ala	Val	Ala	Glu	Val	Leu	
			20					25					30			
gaa	tct	ttg	aag	atc	gtc	ctg	gaa	aag	gac	cct	cat	tac	gct	gat	tac	144
Glu	Ser	Leu	Lys	Ile	Val	Leu	Glu	Lys	Asp	Pro	His	Tyr	Ala	Asp	Tyr	
		35					40					45				
ggg	ctc	atc	cag	cgc	ctg	tgc	gag	cct	gag	cgt	cag	ctc	atc	ttc	cgt	192
Gly	Leu	Ile	Gln	Arg	Leu	Cys	Glu	Pro	Glu	Arg	Gln	Leu	Ile	Phe	Arg	
	50					55				60						
gtg	cct	tgg	ggt	gat	gac	cag	ggc	cag	gtc	cac	gtc	aac	cgt	ggg	ttc	240
Val	Pro	Trp	Val	Asp	Asp	Gln	Gly	Gln	Val	His	Val	Asn	Arg	Gly	Phe	
	65				70					75					80	
cgc	gtg	cag	ttc	aac	tct	gca	ctt	gga	cca	tac	aag	ggc	ggc	ctg	cgc	288
Arg	Val	Gln	Phe	Asn	Ser	Ala	Leu	Gly	Pro	Tyr	Lys	Gly	Gly	Leu	Arg	
				85					90					95		
ttc	cac	cca	tct	gta	aac	ctg	ggc	att	gtg	aag	ttc	ctg	ggc	ttt	gag	336
Phe	His	Pro	Ser	Val	Asn	Leu	Gly	Ile	Val	Lys	Phe	Leu	Gly	Phe	Glu	
			100					105					110			
cag	atc	ttt	aaa	aac	tcc	cta	acc	ggc	ctg	cca	atc	ggg	ggg	ggc	aag	384
Gln	Ile	Phe	Lys	Asn	Ser	Leu	Thr	Gly	Leu	Pro	Ile	Gly	Gly	Gly	Lys	
		115					120					125				
ggg	gga	tcc	gac	ttc	gac	cct	aag	ggc	aag	tcc	gat	ctg	gaa	atc	atg	432
Gly	Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Asp	Leu	Glu	Ile	Met	
	130					135					140					
cgt	ttc	tgc	cag	tcc	ttc	atg	acc	gag	ctg	cac	cgc	cac	atc	ggg	gag	480
Arg	Phe	Cys	Gln	Ser	Phe	Met	Thr	Glu	Leu	His	Arg	His	Ile	Gly	Glu	
	145				150					155					160	
tac	cgc	gac	gtt	cct	gca	ggg	gac	atc	gga	gtt	ggg	ggc	cgc	gag	atc	528
Tyr	Arg	Asp	Val	Pro	Ala	Gly	Asp	Ile	Gly	Val	Gly	Gly	Arg	Glu	Ile	
				165					170					175		
ggg	tac	ctg	ttt	ggc	cac	tac	cgt	cgc	atg	gct	aac	cag	cac	gag	tcc	576
Gly	Tyr	Leu	Phe	Gly	His	Tyr	Arg	Arg	Met	Ala	Asn	Gln	His	Glu	Ser	
			180					185					190			
ggc	gtt	ttg	acc	ggg	aag	ggc	ctg	acc	tgg	ggg	gga	tcc	ctg	gtc	cgc	624
Gly	Val	Leu	Thr	Gly	Lys	Gly	Leu	Thr	Trp	Gly	Gly	Ser	Leu	Val	Arg	
		195					200					205				
acc	gag	gca	act	ggc	tac	ggc	tgc	gtt	tac	ttc	gtg	agt	gaa	atg	atc	672
Thr	Glu	Ala	Thr	Gly	Tyr	Gly	Cys	Val	Tyr	Phe	Val	Ser	Glu	Met	Ile	
	210					215					220					
aag	gct	aag	ggc	gag	agc	atc	agc	ggc	cag	aag	atc	atc	gtt	tcc	ggg	720
Lys	Ala	Lys	Gly	Glu	Ser	Ile	Ser	Gly	Gln	Lys	Ile	Ile	Val	Ser	Gly	
	225				230					235					240	
tcc	ggc	aac	gta	gca	acc	tac	gcg	att	gaa	aag	gct	cag	gaa	ctc	ggc	768

Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Glu	Lys	Ala	Gln	Glu	Leu	Gly	
				245					250					255		
gca	acc	gtt	att	ggt	ttc	tcc	gat	tcc	agc	ggg	tgg	gtt	cat	acc	cct	816
Ala	Thr	Val	Ile	Gly	Phe	Ser	Asp	Ser	Ser	Gly	Trp	Val	His	Thr	Pro	
			260					265					270			
aac	ggc	gtt	gac	gtg	gct	aag	ctc	cgc	gaa	atc	aag	gaa	gtt	cgc	cgc	864
Asn	Gly	Val	Asp	Val	Ala	Lys	Leu	Arg	Glu	Ile	Lys	Glu	Val	Arg	Arg	
		275					280					285				
gca	cgc	gta	tcc	gtg	tac	gcc	gac	gaa	att	gaa	ggc	gca	acc	tac	cac	912
Ala	Arg	Val	Ser	Val	Tyr	Ala	Asp	Glu	Ile	Glu	Gly	Ala	Thr	Tyr	His	
	290					295					300					
acc	gac	ggg	tcc	atc	tgg	gat	ctc	aag	tgc	gat	atc	gct	ctt	cct	tgt	960
Thr	Asp	Gly	Ser	Ile	Trp	Asp	Leu	Lys	Cys	Asp	Ile	Ala	Leu	Pro	Cys	
305				310					315						320	
gca	act	cag	aac	gag	ctc	aac	ggc	gag	aac	gct	aag	act	ctt	gca	gac	1008
Ala	Thr	Gln	Asn	Glu	Leu	Asn	Gly	Glu	Asn	Ala	Lys	Thr	Leu	Ala	Asp	
			325					330						335		
aac	ggc	tgc	cgt	ttc	gtt	gct	gaa	ggc	gcg	aac	atg	cct	tcc	acc	cct	1056
Asn	Gly	Cys	Arg	Phe	Val	Ala	Glu	Gly	Ala	Asn	Met	Pro	Ser	Thr	Pro	
			340					345					350			
gag	gct	gtt	gag	gtc	ttc	cgt	gag	cgc	gac	atc	cgc	ttc	gga	cca	ggc	1104
Glu	Ala	Val	Glu	Val	Phe	Arg	Glu	Arg	Asp	Ile	Arg	Phe	Gly	Pro	Gly	
		355					360					365				
aag	gca	gct	aac	gct	ggg	gtt	gca	acc	tcc	gct	ctg	gag	atg	cag		1152
Lys	Ala	Ala	Asn	Ala	Gly	Gly	Val	Ala	Thr	Ser	Ala	Leu	Glu	Met	Gln	
	370				375						380					
cag	aac	gct	tcg	cgc	gat	tcc	tgg	agc	ttc	gag	tac	acc	gac	gag	cgc	1200
Gln	Asn	Ala	Ser	Arg	Asp	Ser	Trp	Ser	Phe	Glu	Tyr	Thr	Asp	Glu	Arg	
385				390					395						400	
ctc	cag	gtg	atc	atg	aag	aac	atc	ttc	aag	acc	tgt	gca	gag	acc	gca	1248
Leu	Gln	Val	Ile	Met	Lys	Asn	Ile	Phe	Lys	Thr	Cys	Ala	Glu	Thr	Ala	
			405					410					415			
gca	gag	tat	gga	cac	gag	aac	gat	tac	gtt	gtc	ggc	gct	aac	att	gct	1296
Ala	Glu	Tyr	Gly	His	Glu	Asn	Asp	Tyr	Val	Val	Gly	Ala	Asn	Ile	Ala	
			420				425					430				
ggc	ttt	aag	aag	gta	gct	gac	gcg	atg	ctg	gca	cag	ggc	gtc	atc	taa	1344
Gly	Phe	Lys	Lys	Val	Ala	Asp	Ala	Met	Leu	Ala	Gln	Gly	Val	Ile		
		435					440					445				

<210> 82

<211> 447

<212> PRT

<213> Brevibacterium lactofermentum

<400> 82

Met	Thr	Val	Asp	Glu	Gln	Val	Ser	Asn	Tyr	Tyr	Asp	Met	Leu	Leu	Lys
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Arg	Asn	Ala	Gly	Glu	Pro	Glu	Phe	His	Gln	Ala	Val	Ala	Glu	Val	Leu
		20					25					30			
Glu	Ser	Leu	Lys	Ile	Val	Leu	Glu	Lys	Asp	Pro	His	Tyr	Ala	Asp	Tyr
		35					40					45			

Gly	Leu	Ile	Gln	Arg	Leu	Cys	Glu	Pro	Glu	Arg	Gln	Leu	Ile	Phe	Arg
50						55					60				
Val	Pro	Trp	Val	Asp	Asp	Gln	Gly	Gln	Val	His	Val	Asn	Arg	Gly	Phe
65					70					75					80
Arg	Val	Gln	Phe	Asn	Ser	Ala	Leu	Gly	Pro	Tyr	Lys	Gly	Gly	Leu	Arg
				85					90					95	
Phe	His	Pro	Ser	Val	Asn	Leu	Gly	Ile	Val	Lys	Phe	Leu	Gly	Phe	Glu
			100					105					110		
Gln	Ile	Phe	Lys	Asn	Ser	Leu	Thr	Gly	Leu	Pro	Ile	Gly	Gly	Gly	Lys
		115						120				125			
Gly	Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Asp	Leu	Glu	Ile	Met
130						135					140				
Arg	Phe	Cys	Gln	Ser	Phe	Met	Thr	Glu	Leu	His	Arg	His	Ile	Gly	Glu
145					150					155					160
Tyr	Arg	Asp	Val	Pro	Ala	Gly	Asp	Ile	Gly	Val	Gly	Gly	Arg	Glu	Ile
			165						170					175	
Gly	Tyr	Leu	Phe	Gly	His	Tyr	Arg	Arg	Met	Ala	Asn	Gln	His	Glu	Ser
			180				185					190			
Gly	Val	Leu	Thr	Gly	Lys	Gly	Leu	Thr	Trp	Gly	Gly	Ser	Leu	Val	Arg
	195						200					205			
Thr	Glu	Ala	Thr	Gly	Tyr	Gly	Cys	Val	Tyr	Phe	Val	Ser	Glu	Met	Ile
210						215					220				
Lys	Ala	Lys	Gly	Glu	Ser	Ile	Ser	Gly	Gln	Lys	Ile	Ile	Val	Ser	Gly
225					230					235					240
Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Glu	Lys	Ala	Gln	Glu	Leu	Gly
			245						250					255	
Ala	Thr	Val	Ile	Gly	Phe	Ser	Asp	Ser	Ser	Gly	Trp	Val	His	Thr	Pro
			260					265					270		
Asn	Gly	Val	Asp	Val	Ala	Lys	Leu	Arg	Glu	Ile	Lys	Glu	Val	Arg	Arg
	275						280					285			
Ala	Arg	Val	Ser	Val	Tyr	Ala	Asp	Glu	Ile	Glu	Gly	Ala	Thr	Tyr	His
290						295					300				
Thr	Asp	Gly	Ser	Ile	Trp	Asp	Leu	Lys	Cys	Asp	Ile	Ala	Leu	Pro	Cys
305					310					315					320
Ala	Thr	Gln	Asn	Glu	Leu	Asn	Gly	Glu	Asn	Ala	Lys	Thr	Leu	Ala	Asp
			325						330					335	
Asn	Gly	Cys	Arg	Phe	Val	Ala	Glu	Gly	Ala	Asn	Met	Pro	Ser	Thr	Pro
			340					345					350		
Glu	Ala	Val	Glu	Val	Phe	Arg	Glu	Arg	Asp	Ile	Arg	Phe	Gly	Pro	Gly
	355						360					365			
Lys	Ala	Ala	Asn	Ala	Gly	Gly	Val	Ala	Thr	Ser	Ala	Leu	Glu	Met	Gln
370						375					380				
Gln	Asn	Ala	Ser	Arg	Asp	Ser	Trp	Ser	Phe	Glu	Tyr	Thr	Asp	Glu	Arg
385					390					395					400
Leu	Gln	Val	Ile	Met	Lys	Asn	Ile	Phe	Lys	Thr	Cys	Ala	Glu	Thr	Ala
			405						410					415	
Ala	Glu	Tyr	Gly	His	Glu	Asn	Asp	Tyr	Val	Val	Gly	Ala	Asn	Ile	Ala
			420					425					430		
Gly	Phe	Lys	Lys	Val	Ala	Asp	Ala	Met	Leu	Ala	Gln	Gly	Val	Ile	
	435						440					445			

<210> 83
 <211> 20
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer for
 amplifying gltA gene

 <220>
 <221> misc_feature
 <222> (9)..(9)
 <223> n = inosine

 <400> 83
 aagatcacnt acatcgaygg 20

 <210> 84
 <211> 20
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer for
 amplifying gltA gene

 <400> 84
 tagaagtcta cgttcgggta 20

 <210> 85
 <211> 21
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer for
 amplifying gltA gene

 <400> 85
 gtcgacaata gcctgaatct g 21

 <210> 86
 <211> 21
 <212> DNA

 <213> Artificial Sequence

 <220>

<223> Description of Artificial Sequence:primer for
amplifying gltA gene

<400> 86
cggtggaacc ggtgctgaca t 21

<210> 87
<211> 21
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying gltA gene

<400> 87
gggtgggga attcggtcatg t 21

<210> 88
<211> 21
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying gltA gene

<400> 88
tgtcgtagcc gcggtagcgc a 21

<210> 89
<211> 1293
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(1290)

<400> 89
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Val Ala Ser Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu
1 5 10 15
ttc gag atg ggc atc aag cag gcc acc gag ggt aac tcc ggt gtc atc 96
Phe Glu Met Gly Ile Lys Gln Ala Thr Glu Gly Asn Ser Gly Val Ile
20 25 30
ctg ggt aag atg ctg tcg gaa acc ggt ctg gtc acc ttc gac ccc ggt 144
Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Val Thr Phe Asp Pro Gly
35 40 45

tat gtc agc acc ggt tcc acc gaa tcc aag atc acc tac atc gat ggt	192
Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly	
50 55 60	
gat gca ggc atc ctg cgc tac cgc ggc tac gac att gcg gat ctg gcc	240
Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala	
65 70 75 80	
gaa aat gcc acc ttc aat gag gtc tcc tac ctc ctg atc aag ggt gag	288
Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Lys Gly Glu	
85 90 95	
ctc ccg acc ccg gaa gag ctc cac aag ttc aac gac gag att cgt cac	336
Leu Pro Thr Pro Glu Glu Leu His Lys Phe Asn Asp Glu Ile Arg His	
100 105 110	
cac acc ctg ctg gac gag gac ttc aag tcc cag ttc aat gtc ttc cct	384
His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro	
115 120 125	
cgc gat gcc cac ccg atg gcc acc ctg gcc tcc tcg gtt aac atc ctc	432
Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu	
130 135 140	
tcc acc tac tac cag gat cag ctg gat ccc ctg gat gag gct cag ctg	480
Ser Thr Tyr Tyr Gln Asp Gln Leu Asp Pro Leu Asp Glu Ala Gln Leu	
145 150 155 160	
gac aag gca acc gtc cgc ctg atg gcg aag gtt ccg atg ctg gct gca	528
Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala	
165 170 175	
tac gca cac cgt gcc cgc aag ggt gcg ccg tac atg tac ccg gac aac	576
Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn	
180 185 190	
tcc ctc aat gcc cgt gag aac ttc ctg cgc atg atg ttc ggt tac ccg	624
Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro	
195 200 205	
acc gag ccg tac gag gtt gat ccg atc atg gtc aaa gcc ctc gac aag	672
Thr Glu Pro Tyr Glu Val Asp Pro Ile Met Val Lys Ala Leu Asp Lys	
210 215 220	
ctg ctc atc ctg cac gca gac cac gag cag aac tgc tcc acc tcc act	720
Leu Leu Ile Leu His Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr	
225 230 235 240	
gtc cgc atg atc ggc tcc gcg cag gcg aac atg ttc gtc tcc atc gcc	768
Val Arg Met Ile Gly Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala	
245 250 255	
ggc ggc atc aac gca ctc tcc ggc ccg ctg cac ggt ggc gcc aac cag	816
Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln	
260 265 270	
gct gtc ctc gag atg ctc gag gag atc gca gcc aac ggc ggc gac gca	864
Ala Val Leu Glu Met Leu Glu Glu Ile Ala Ala Asn Gly Gly Asp Ala	
275 280 285	
acc gac ttc atg aac cgc gtg aag aac aag gag aag ggt gtc cgc ctc	912
Thr Asp Phe Met Asn Arg Val Lys Asn Lys Glu Lys Gly Val Arg Leu	
290 295 300	
atg ggc ttc gga cac cgc gtc tac aag aac tac gat ccg cgt gca gcc	960
Met Gly Phe Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Ala	
305 310 315 320	

atc gtc aag gac acc gcc cac gag atc ctc gag cac ctc ggt ggc gac	1008
Ile Val Lys Asp Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp	
325 330 335	
cca ctg ctg gat ctg gct ctc aag ctg gaa gaa atc gca ctc aac gac	1056
Pro Leu Leu Asp Leu Ala Leu Lys Leu Glu Glu Ile Ala Leu Asn Asp	
340 345 350	
gat tac ttc atc tcc cgc aag ctg tac ccg aac gtg gac ttc tac acc	1104
Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr	
355 360 365	
ggc ctg atc tac cgc gcc atg ggc ttc ccg acg gac ttc ttc acc gtc	1152
Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val	
370 375 380	
ctg ttc gcc atc ggc cgc ctc ccg ggc tgg atc gcc cac tac cgc gag	1200
Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu	
385 390 395 400	
cag ctc gcc gat ccg ggc gcc aag atc aac cgt cct cgc cag atc tac	1248
Gln Leu Ala Asp Pro Gly Ala Lys Ile Asn Arg Pro Arg Gln Ile Tyr	
405 410 415	
acc ggt gag acc gca cgc aag atc atc ccc cgc gaa gag cgc tag	1293
Thr Gly Glu Thr Ala Arg Lys Ile Ile Pro Arg Glu Glu Arg	
420 425 430	

<210> 90

<211> 430

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 90

Val Ala Ser Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu	
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Phe Glu Met Gly Ile Lys Gln Ala Thr Glu Gly Asn Ser Gly Val Ile	
20 25 30	
Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Val Thr Phe Asp Pro Gly	
35 40 45	
Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly	
50 55 60	
Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala	
65 70 75 80	
Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Lys Gly Glu	
85 90 95	
Leu Pro Thr Pro Glu Glu Leu His Lys Phe Asn Asp Glu Ile Arg His	
100 105 110	
His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro	
115 120 125	
Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu	
130 135 140	
Ser Thr Tyr Tyr Gln Asp Gln Leu Asp Pro Leu Asp Glu Ala Gln Leu	
145 150 155 160	
Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala	
165 170 175	
Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn	

			180					185					190			
Ser	Leu	Asn	Ala	Arg	Glu	Asn	Phe	Leu	Arg	Met	Met	Phe	Gly	Tyr	Pro	
		195					200					205				
Thr	Glu	Pro	Tyr	Glu	Val	Asp	Pro	Ile	Met	Val	Lys	Ala	Leu	Asp	Lys	
	210					215					220					
Leu	Leu	Ile	Leu	His	Ala	Asp	His	Glu	Gln	Asn	Cys	Ser	Thr	Ser	Thr	
225					230					235					240	
Val	Arg	Met	Ile	Gly	Ser	Ala	Gln	Ala	Asn	Met	Phe	Val	Ser	Ile	Ala	
				245					250					255		
Gly	Gly	Ile	Asn	Ala	Leu	Ser	Gly	Pro	Leu	His	Gly	Gly	Ala	Asn	Gln	
			260					265					270			
Ala	Val	Leu	Glu	Met	Leu	Glu	Glu	Ile	Ala	Ala	Asn	Gly	Gly	Asp	Ala	
	275						280					285				
Thr	Asp	Phe	Met	Asn	Arg	Val	Lys	Asn	Lys	Glu	Lys	Gly	Val	Arg	Leu	
	290					295					300					
Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys	Asn	Tyr	Asp	Pro	Arg	Ala	Ala	
305					310				315						320	
Ile	Val	Lys	Asp	Thr	Ala	His	Glu	Ile	Leu	Glu	His	Leu	Gly	Gly	Asp	
				325				330					335			
Pro	Leu	Leu	Asp	Leu	Ala	Leu	Lys	Leu	Glu	Glu	Ile	Ala	Leu	Asn	Asp	
			340					345					350			
Asp	Tyr	Phe	Ile	Ser	Arg	Lys	Leu	Tyr	Pro	Asn	Val	Asp	Phe	Tyr	Thr	
	355					360						365				
Gly	Leu	Ile	Tyr	Arg	Ala	Met	Gly	Phe	Pro	Thr	Asp	Phe	Phe	Thr	Val	
	370				375						380					
Leu	Phe	Ala	Ile	Gly	Arg	Leu	Pro	Gly	Trp	Ile	Ala	His	Tyr	Arg	Glu	
385					390					395					400	
Gln	Leu	Ala	Asp	Pro	Gly	Ala	Lys	Ile	Asn	Arg	Pro	Arg	Gln	Ile	Tyr	
				405				410					415			
Thr	Gly	Glu	Thr	Ala	Arg	Lys	Ile	Ile	Pro	Arg	Glu	Glu	Arg			
			420					425					430			

<210> 91
 <211> 1314
 <212> DNA
 <213> Brevibacterium lactofermentum

<220>
 <221> CDS
 <222> (1)..(1311)

<400> 91																
atg	ttt	gaa	agg	gat	atc	gtg	gct	act	gat	aac	aac	aag	gct	gtc	ctg	48
Met	Phe	Glu	Arg	Asp	Ile	Val	Ala	Thr	Asp	Asn	Asn	Lys	Ala	Val	Leu	
1				5				10					15			
cac	tac	ccc	ggg	ggc	gag	ttc	gaa	atg	gac	atc	atc	gag	gct	tct	gag	96
His	Tyr	Pro	Gly	Gly	Glu	Phe	Glu	Met	Asp	Ile	Ile	Glu	Ala	Ser	Glu	
			20					25				30				
ggg	aac	aac	ggg	ggt	gtc	ctg	ggc	aag	atg	ctg	tct	gag	act	gga	ctg	144
Gly	Asn	Asn	Gly	Val	Val	Leu	Gly	Lys	Met	Leu	Ser	Glu	Thr	Gly	Leu	
	35						40					45				

atc	act	ttt	gac	cca	ggt	tat	gtg	agc	act	ggc	tcc	acc	gag	tcg	aag	192
Ile	Thr	Phe	Asp	Pro	Gly	Tyr	Val	Ser	Thr	Gly	Ser	Thr	Glu	Ser	Lys	
50						55					60					
atc	acc	tac	atc	gat	ggc	gat	gcg	gga	atc	ctg	cgt	tac	cgc	ggc	tat	240
Ile	Thr	Tyr	Ile	Asp	Gly	Asp	Ala	Gly	Ile	Leu	Arg	Tyr	Arg	Gly	Tyr	
65					70					75					80	
gac	atc	gct	gat	ctg	gct	gag	aat	gcc	acc	ttc	aac	gag	gtt	tct	tac	288
Asp	Ile	Ala	Asp	Leu	Ala	Glu	Asn	Ala	Thr	Phe	Asn	Glu	Val	Ser	Tyr	
				85					90					95		
cta	ctt	atc	aac	ggt	gaa	cta	cca	acc	cca	gat	gag	ctt	cac	aag	ttt	336
Leu	Leu	Ile	Asn	Gly	Glu	Leu	Pro	Thr	Pro	Asp	Glu	Leu	His	Lys	Phe	
			100					105					110			
aac	gac	gag	att	cgc	cac	cac	acc	ctt	ctg	gac	gag	gac	ttc	aag	tcc	384
Asn	Asp	Glu	Ile	Arg	His	His	Thr	Leu	Leu	Asp	Glu	Asp	Phe	Lys	Ser	
		115					120					125				
cag	ttc	aac	gtg	ttc	cca	cgc	gac	gct	cac	cca	atg	gca	acc	ttg	gct	432
Gln	Phe	Asn	Val	Phe	Pro	Arg	Asp	Ala	His	Pro	Met	Ala	Thr	Leu	Ala	
	130					135					140					
tcc	tcg	gtt	aac	att	ttg	tct	acc	tac	tac	cag	gat	cag	ctg	aac	cca	480
Ser	Ser	Val	Asn	Ile	Leu	Ser	Thr	Tyr	Tyr	Gln	Asp	Gln	Leu	Asn	Pro	
145					150					155					160	
ctc	gat	gag	gca	cag	ctt	gat	aag	gca	acc	gtt	cgc	ctc	atg	gca	aag	528
Leu	Asp	Glu	Ala	Gln	Leu	Asp	Lys	Ala	Thr	Val	Arg	Leu	Met	Ala	Lys	
				165					170					175		
gtt	cca	atg	ctg	gct	gcg	tac	gca	cac	cgc	gca	cgc	aag	ggt	gct	cct	576
Val	Pro	Met	Leu	Ala	Ala	Tyr	Ala	His	Arg	Ala	Arg	Lys	Gly	Ala	Pro	
			180					185					190			
tac	atg	tac	cca	gac	aac	tcc	ctc	aac	gcg	cgt	gag	aac	ttc	ctg	cgc	624
Tyr	Met	Tyr	Pro	Asp	Asn	Ser	Leu	Asn	Ala	Arg	Glu	Asn	Phe	Leu	Arg	
		195					200					205				
atg	atg	ttc	ggt	tac	cca	acc	gag	cca	tac	gag	atc	gac	cca	atc	atg	672
Met	Met	Phe	Gly	Tyr	Pro	Thr	Glu	Pro	Tyr	Glu	Ile	Asp	Pro	Ile	Met	
	210					215					220					
gtc	aag	gct	ctg	gac	aag	ctg	ctc	atc	ctg	cac	gct	gac	cac	gag	cag	720
Val	Lys	Ala	Leu	Asp	Lys	Leu	Leu	Ile	Leu	His	Ala	Asp	His	Glu	Gln	
225				230						235					240	
aac	tgc	tcc	acc	tcc	acc	gtt	cgt	atg	atc	ggc	tcc	gca	cag	gcc	aac	768
Asn	Cys	Ser	Thr	Ser	Thr	Val	Arg	Met	Ile	Gly	Ser	Ala	Gln	Ala	Asn	
				245				250						255		
atg	ttt	gtc	tcc	atc	gct	ggt	ggc	atc	aac	gct	ctg	tcc	ggc	cca	ctg	816
Met	Phe	Val	Ser	Ile	Ala	Gly	Gly	Ile	Asn	Ala	Leu	Ser	Gly	Pro	Leu	
			260				265						270			
cac	ggt	ggc	gca	aac	cag	gct	gtt	ctg	gag	atg	ctc	gaa	gac	atc	aag	864
His	Gly	Gly	Ala	Asn	Gln	Ala	Val	Leu	Glu	Met	Leu	Glu	Asp	Ile	Lys	
		275					280					285				
aac	aac	cac	ggt	ggc	gac	gca	acc	gcg	ttc	atg	aac	aag	gtc	aag	aac	912
Asn	Asn	His	Gly	Gly	Asp	Ala	Thr	Ala	Phe	Met	Asn	Lys	Val	Lys	Asn	
	290				295						300					
aag	gaa	gac	ggc	gtc	cgc	ctc	atg	ggc	ttc	gga	cac	cgc	gtt	tac	aag	960
Lys	Glu	Asp	Gly	Val	Arg	Leu	Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys	
305					310					315					320	

aac tac gat cca cgt gca gca atc gtc aag gag acc gca cac gag atc	1008
Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu Thr Ala His Glu Ile	
325 330 335	
ctc gag cac ctc ggt ggc gac gat ctt ctg gat ctg gca atc aag ctg	1056
Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu	
340 345 350	
gaa gaa att gca ctg gct gat gat tac ttc atc tcc cgc aag ctc tac	1104
Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr	
355 360 365	
ccg aac gta gac ttc tac acc ggc ctg atc tac cgc gca atg ggc ttc	1152
Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe	
370 375 380	
cca act gac ttc ttc acc gta ttg ttc gca atc ggt cgt ctg cca gga	1200
Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile Gly Arg Leu Pro Gly	
385 390 395 400	
tgg atc gct cac tac cgc gag cag ctc ggt gca gca ggc aac aag atc	1248
Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile	
405 410 415	
aac cgc cca cgc cag gtc tac acc ggc aag gaa tcc cgc aag ttg gtt	1296
Asn Arg Pro Arg Gln Val Tyr Thr Gly Lys Glu Ser Arg Lys Leu Val	
420 425 430	
cct cgc gag gag cgc taa	1314
Pro Arg Glu Glu Arg	
435	

<210> 92

<211> 437

<212> PRT

<213> Brevibacterium lactofermentum

<400> 92

Met Phe Glu Arg Asp Ile Val Ala Thr Asp Asn Asn Lys Ala Val Leu	
1 5 10 15	
His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile Ile Glu Ala Ser Glu	
20 25 30	
Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu Ser Glu Thr Gly Leu	
35 40 45	
Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys	
50 55 60	
Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr	
65 70 75 80	
Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr	
85 90 95	
Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp Glu Leu His Lys Phe	
100 105 110	
Asn Asp Glu Ile Arg His His Thr Leu Leu Asp Glu Asp Phe Lys Ser	
115 120 125	
Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro Met Ala Thr Leu Ala	
130 135 140	
Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro	
145 150 155 160	

Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val Arg Leu Met Ala Lys
 165 170 175
 Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala Arg Lys Gly Ala Pro
 180 185 190
 Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg
 195 200 205
 Met Met Phe Gly Tyr Pro Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met
 210 215 220
 Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His Ala Asp His Glu Gln
 225 230 235 240
 Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly Ser Ala Gln Ala Asn
 245 250 255
 Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu
 260 265 270
 His Gly Gly Ala Asn Gln Ala Val Leu Glu Met Leu Glu Asp Ile Lys
 275 280 285
 Asn Asn His Gly Gly Asp Ala Thr Ala Phe Met Asn Lys Val Lys Asn
 290 295 300
 Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly His Arg Val Tyr Lys
 305 310 315 320
 Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu Thr Ala His Glu Ile
 325 330 335
 Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu
 340 345 350
 Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr
 355 360 365
 Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe
 370 375 380
 Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile Gly Arg Leu Pro Gly
 385 390 395 400
 Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile
 405 410 415
 Asn Arg Pro Arg Gln Val Tyr Thr Gly Lys Glu Ser Arg Lys Leu Val
 420 425 430
 Pro Arg Glu Glu Arg
 435

<210> 93

<211> 1656

<212> DNA

<213> *Corynebacterium thermoaminogenes*

<220>

<221> CDS

<222> (309)..(1595)

<400> 93

acgcccgatt cttcaacact atcgaagagg tcccaaccca cgcgttgacc cagggttgg 60
 gtactttgtc ccgcgcgcaa aatatcgtgt tgggtggcaac tggccaagga aaagcagaca 120
 gccatccgcg gaactgtgga aggtccagtg actgcttctt gcccagggtt cattctgcaa 180
 atgcacaaca acgccaccat catcgttgat gaagcagcag catccaagct gaaaaatgct 240

gaccattacc gtctcatgga gcaattaaag ctgctgtaga aacaaaaagg aaagtactgt 300
gtgggggct atg cac aca gaa ctt tcc agt ttg cgc cct gcg tac cat gtg 350
Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val
1 5 10
act cct ccg cag ggc aga ctc aat gat ccc aat gga atg tac gtc gat 398
Thr Pro Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp
15 20 25 30
gga gat acc ctc cac gtc tac tac cag cac gat cca ggt ttc ccc ttc 446
Gly Asp Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe
35 40 45
gca cca aag cgc acc ggt tgg gct cac acc acc acg ccg ttg acc gga 494
Ala Pro Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly
50 55 60
ccg cag cga ttg cag tgg acg cac ctg ccc gat gct ctt tac ccg gat 542
Pro Gln Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp
65 70 75
gta tcc tat gac ctg gat gga tgc tat tcc ggc gga gcc gta ttt tct 590
Val Ser Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser
80 85 90
gac ggc acg ctt aaa ctt ttc tac acc ggc aac cga aaa att gac ggc 638
Asp Gly Thr Leu Lys Leu Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly
95 100 105 110
aag cgc cgc gcc acc caa aac ctc gtc gaa gtc gag gac cca act ggg 686
Lys Arg Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly
115 120 125
ctg atg ggc ggc att cat cgc cgc tcg cct aaa aat ccg ctt atc gac 734
Leu Met Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp
130 135 140
gga ccc gcc agc ggt ttt acg ccc cac tac cgc gat ccc atg atc agc 782
Gly Pro Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser
145 150 155
cct gat ggg gat ggt tgg aag atg gtt ctt ggg gct cag cgc gaa aac 830
Pro Asp Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn
160 165 170
ctc acc ggt gca gcg gtt cta tac cgc tcg gca gat ctt gaa aac tgg 878
Leu Thr Gly Ala Ala Val Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp
175 180 185 190
gaa ttc tcc ggt gaa atc acc ttt gac ctc agc gac gca caa cct ggt 926
Glu Phe Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly
195 200 205
tct gcc cct gat ctc gtt cct ggc ggc tac atg tgg gaa tgc ccc aac 974
Ser Ala Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn
210 215 220
ctt ttt acg ctt cgc gat gaa aaa acc ggc gaa gac ctc gat gtg ctg 1022
Leu Phe Thr Leu Arg Asp Glu Lys Thr Gly Glu Asp Leu Asp Val Leu
225 230 235
att ttc tgt cca caa gga ttg gac cgt atc gat gat gag gtt act cac 1070
Ile Phe Cys Pro Gln Gly Leu Asp Arg Ile Asp Asp Glu Val Thr His
240 245 250
tac gca agc tct gac cag tgc gga tat gtc gtc ggc aag ctt gaa gaa 1118
Tyr Ala Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Glu

255		260		265		270	
acg acc ttc cgt gtc	ctg cga gga ttc agc gag	ctg gat ttc ggt cat	1166				
Thr Thr Phe Arg Val	Leu Arg Gly Phe Ser Glu	Leu Asp Phe Gly His					
	275	280	285				
gaa ttc tac gcg ccg	cag gtt gca gtc aac ggt	tcc gat gcc tgg ctt	1214				
Glu Phe Tyr Ala Pro	Gln Val Ala Val Asn Gly	Ser Asp Ala Trp Leu					
	290	295	300				
gtg ggc tgg atg gga	ttg cct gca cag gat	gat cac cca aca gtt	gcg 1262				
Val Gly Trp Met Gly	Leu Pro Ala Gln Asp	Asp His Pro Thr Val	Ala				
	305	310	315				
cag gaa gga tgg gtg	cac tgc ctg acc gtt	cct cgc agg ctt cat	ttg 1310				
Gln Glu Gly Trp Val	His Cys Leu Thr Val	Pro Arg Arg Leu His	Leu				
	320	325	330				
cgt aac cat gcg atc	tat caa gag ctt ctt	ctc cca gaa ggg gag	tcg 1358				
Arg Asn His Ala Ile	Tyr Gln Glu Leu Leu	Leu Pro Glu Gly Glu	Ser				
	335	340	345				
ggg gta act aga tct	gta tta ggt tct gaa	cct gtc cga gta gac	atc 1406				
Gly Val Thr Arg Ser	Val Leu Gly Ser Glu	Pro Val Arg Val Asp	Ile				
	355	360	365				
cga gac aat gtt tcc	ctc gag tgg gat ggt	gtc cgg ttg tct gtg	gat 1454				
Arg Asp Asn Val Ser	Leu Glu Trp Asp Gly	Val Arg Leu Ser Val	Asp				
	370	375	380				
cgc gat ggc gat cgt	cgt gta gct gaa gta	aaa cct ggc gaa tta	gtg 1502				
Arg Asp Gly Asp Arg	Arg Val Ala Glu Val	Lys Pro Gly Glu Leu	Val				
	385	390	395				
atc gcg gac gat aat	aca gcg att gag ata	aca gca ggt cat ggc	cag 1550				
Ile Ala Asp Asp Asn	Thr Ala Ile Glu Ile	Thr Ala Gly His Gly	Gln				
	400	405	410				
gtt tcc ttc gct ttc	cgc acc ttc aaa ggt	gac act att gag aga	1595				
Val Ser Phe Ala Phe	Arg Thr Phe Lys Gly	Asp Thr Ile Glu Arg					
	415	420	425				
taagtcataa aaaagggcct tctgtggcgg attgtacaaa tacttcgcaa aatcccttga 1655							
t 1656							

<210> 94
 <211> 429
 <212> PRT
 <213> Corynebacterium thermoaminogenes

<400> 94
 Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro
 1 5 10 15
 Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp
 20 25 30
 Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro
 35 40 45
 Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln
 50 55 60
 Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser
 65 70 75 80
 Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly

				85				90					95			
Thr	Leu	Lys	Leu	Phe	Tyr	Thr	Gly	Asn	Arg	Lys	Ile	Asp	Gly	Lys	Arg	
			100					105					110			
Arg	Ala	Thr	Gln	Asn	Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	
		115					120					125				
Gly	Gly	Ile	His	Arg	Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	
	130					135					140					
Ala	Ser	Gly	Phe	Thr	Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	
145					150					155					160	
Gly	Asp	Gly	Trp	Lys	Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	
				165					170					175		
Gly	Ala	Ala	Val	Leu	Tyr	Arg	Ser	Ala	Asp	Leu	Glu	Asn	Trp	Glu	Phe	
			180					185					190			
Ser	Gly	Glu	Ile	Thr	Phe	Asp	Leu	Ser	Asp	Ala	Gln	Pro	Gly	Ser	Ala	
	195						200					205				
Pro	Asp	Leu	Val	Pro	Gly	Gly	Tyr	Met	Trp	Glu	Cys	Pro	Asn	Leu	Phe	
	210				215						220					
Thr	Leu	Arg	Asp	Glu	Lys	Thr	Gly	Glu	Asp	Leu	Asp	Val	Leu	Ile	Phe	
225					230					235					240	
Cys	Pro	Gln	Gly	Leu	Asp	Arg	Ile	Asp	Asp	Glu	Val	Thr	His	Tyr	Ala	
				245					250					255		
Ser	Ser	Asp	Gln	Cys	Gly	Tyr	Val	Val	Gly	Lys	Leu	Glu	Glu	Thr	Thr	
			260					265					270			
Phe	Arg	Val	Leu	Arg	Gly	Phe	Ser	Glu	Leu	Asp	Phe	Gly	His	Glu	Phe	
	275						280					285				
Tyr	Ala	Pro	Gln	Val	Ala	Val	Asn	Gly	Ser	Asp	Ala	Trp	Leu	Val	Gly	
	290					295					300					
Trp	Met	Gly	Leu	Pro	Ala	Gln	Asp	Asp	His	Pro	Thr	Val	Ala	Gln	Glu	
305					310					315					320	
Gly	Trp	Val	His	Cys	Leu	Thr	Val	Pro	Arg	Arg	Leu	His	Leu	Arg	Asn	
				325					330					335		
His	Ala	Ile	Tyr	Gln	Glu	Leu	Leu	Leu	Pro	Glu	Gly	Glu	Ser	Gly	Val	
			340					345					350			
Thr	Arg	Ser	Val	Leu	Gly	Ser	Glu	Pro	Val	Arg	Val	Asp	Ile	Arg	Asp	
	355						360					365				
Asn	Val	Ser	Leu	Glu	Trp	Asp	Gly	Val	Arg	Leu	Ser	Val	Asp	Arg	Asp	
	370					375					380					
Gly	Asp	Arg	Arg	Val	Ala	Glu	Val	Lys	Pro	Gly	Glu	Leu	Val	Ile	Ala	
385					390					395					400	
Asp	Asp	Asn	Thr	Ala	Ile	Glu	Ile	Thr	Ala	Gly	His	Gly	Gln	Val	Ser	
				405					410					415		
Phe	Ala	Phe	Arg	Thr	Phe	Lys	Gly	Asp	Thr	Ile	Glu	Arg				
			420					425								

<210> 95

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying scrB gene

<400> 95
gtacatattg tcgttagaac gcgtaatacg actca

35

<210> 96
<211> 35
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying scrB gene

<400> 96
cgttagaacg cgtaatacga ctcactatag ggaga

35

<210> 97
<211> 30
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
LA cloning of scrB

<400> 97
gtaaagagcg tcgggcaggt gcgtccactg

30

<210> 98
<211> 30
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
LA cloning of scrB

<400> 98
ggtgtgagcc cagccggtgc gctttggtgc

30

<210> 99
<211> 30
<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer for
 LA cloning of scrB

 <400> 99
 atcagccctg atggtgatgg ttggaaaatg 30

 <210> 100
 <211> 30
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer for
 LA cloning of scrB gene

 <400> 100
 ggtgcagcgg ttctataccg ctcgacagat 30

 <210> 101
 <211> 32
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer for
 amplifying scrB gene

 <400> 101
 ggcccgggac gcccgattct tcaacactat cg 32

 <210> 102
 <211> 32
 <212> DNA

 <213> Artificial Sequence

 <220>
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 amplifying scrB gene

 <400> 102
 ggcccgggga tcaagggatt ttgcgaagta tt 32

 <210> 103
 <211> 30
 <212> DNA

 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer for
 amplifying icd gene

 <400> 103
 gaagatctct atgaccagcg catcaagctg 30

 <210> 104
 <211> 30
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer for
 amplifying icd gene

 <400> 104
 gaagatctgg tcatcccaga acctgatcac 30

 <210> 105
 <211> 32
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer for
 amplifying gdh gene

 <400> 105
 ggcctgcag gtccgagggt gtgcgttcgg ca 32

 <210> 106
 <211> 32
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer for
 amplifying gdh gene

 <400> 106
 ggcctgcag gcaccaggat gccctcaacc ag 32

 <210> 107
 <211> 30
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying gltA gene

<400> 107

ggggtaccga tcactataac cccacagcac

30

<210> 108

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying gltA gene

<400> 108

ggggtaccct ggctgatctg aactaggcgc

30